## November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases: older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).

rapbm (Published\_Applications\_AA\_New).

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.rge us-10-736-318-22

> 5.1.7 Biocceleration Ltd. GenCore version (c) 1993 - 2006 Copyright

- nucleic search, using sw model OM nucleic

March 7, 2006, 09:04:19 ; Search time 14446 Seconds
(without alignments)
11509.559 Million cell updates/sec Run on:

Title: Perfect score:

US-10-736-318-22 2925 1 gtttggtatttattggatgc......tcaaatttggactaaatctg 2925 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

11766282 5883141 seqs, 28421725653 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

9b ba: \*
9b in: \*
9b om: \*
9b ow: \*
9b ov: \*
9b pat: \*
9b pr: \*
9b w: \*
9b w: \*
9b w: \* GenEmbl:\* 55: 77: 10: 112: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AC021640 Arabidops	AF105034 Arabidops	AF069468 Arabidops	AY088527 Arabidops	AR608874 Sequence	AX573146 Sequence	X90454 A.thaliana	AK176721 Arabidops	AX505726 Sequence	AB231157 Zinnia el	AF081794 Nicotiana	AF099969 Nicotiana	AR237880 Sequence	AR237881 Sequence	BT009523 Triticum	AR237878 Sequence	BT016653 Zea mays	AK111908 Oryza gat
SOFTWANTES	ID	ATAC021640	AF105034	AF069468	AY088527	AR608874	AX573146	ATRNASC5D	AK176721	AX505726	AB231157	AF081794	AF099969	AR237880	AR237881	BT009523	AR237878	BT016653	AK111908
	80	15	15	15	15	9	9	15	15	9	15	15	15	9	9	15	9	15	15
	Query Match Length DB	103904	2294	3004	1163	1175	1175	1175	1113	846	1104	1155	1148	1447	1210	1210	911	1189	1253
dŧ	Query Match	96.9	44.5	31.7	15.9	15.8	15.8	15.8	14.6	11.9	7.8	7.8	7.5	7.0	6.4	6.4	6.4	6.3	6.1
	Score	2835.2	1300.8	926.8	464.2	461	461	461	428.2	347.2	228.2	228	218.8	203.4	188	188	187	184.8	179.6
	Result No.		~	m	4	ហ	9	7	æ	o,	10	11	12	13	14	15	16	17	18

AK112014 Oryza sat AK112014 Oryza sat AK112014 Oryza sat AK137871 Sequence Continuation (19 o AP003214 Oryza sat AK155063 Sequence BT019106 Zea mays BD273096 Materials GT1612 A62988234FM AR249155 Sequence GT1681 A85715834FM BV007175 IS269 Mea AR245020 Sequence AR25209 Sequence AR25209 Sequence I66494 Sequence I66494 Sequence I66494 Sequence I66494 Sequence AC152242 Bos tauru AC19406 Strongylo AC152242 Bos tauru AC19496 Strongylo AR277877 Homo sapi	AJ840631 Arabidops ALI21656 BAC seque AC163195 Bos tauru AC087566 Mus muscu AX346599 Sequence AC104922 Mus muscu
AK137879 AK112014 AK237871 AR237871 AP003207 AP003214 AP003214 AP003216 BD273096 G71612 AR249155 G71681 BV007175 AR245209 166494 AR25209 166494 AC152242 AC152242 AC152242 AC182986 AR237874	AJ840631 CNS01DS6 AC163195 AC087566 AX346599 AC104922
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	14 8 8 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
111 113 288 288 288 288 288 288 288 288 288 28	4 1328 4 179206 4 217543 4 231912 4 340089
	000000 444444
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001020202020202020202020202020202020202	4 4 4 4 4 0 11 2 W 4 12
0 00 0	υυ

## ALIGNMENTS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 103904).C.D., Benito, M.-I., Creasy, T.H., Haas, B., In, D., Roming, C.M., Koo, H., Fujii, C.Y., Utterback, T.R., Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M. Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence Unpublished PLN 30-0CT-2002 9712 9712 ATAC021640 103904 bp DNA linear PLN 30-OCT-Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence, Direct Submission
Submitted (24-JAN-2001) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Jan 24, 2001 this sequence version replaced gi:12280770.
Address all correspondence to:at@tigr.org Submitted (18-JAN-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 103904) Arabidopsis thaliana (thale cress) Arabidopsis thaliana AC021640.7 GI:12408747 2 (bases 1 to 103904) Lin, X. and Kaul, S. Direct Submission complete sequence. Lin, X. VERSION KEYWORDS SOURCE ORGANISM RESULT 1 ATAC021640 LOCUS TITLE JOURNAL REFERENCE AUTHORS AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL ACCESSION REFERENCE COMMENT

BAC clone F16B3 is from Arabidopsis chromosome III and is near the molecular marker mi74. The orientation of the sequence is from SP6 to T7 end of the BAC clone

Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCNNISAFGODPNRIYLMGQSAGAHISSCALFEQAIKESRGESISWSVSQIKAYFGLS
GGYNLFNLVEHFHNRGLYRSIFLSINMGGESSFKQFSFEVRLKOLMVRKAAALLPHILL
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Complement (11800. .14456)
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(http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.iigr.org/tdb/ar/at.hml).
Annotated genes are named to indicate the level of evidence for after the database hits of indicate the significant peptide after the database hits. Genes without significant peptide similarity but with EST similarity to other proteins are named similarity but with EST similarity, that are predicted by more than two gene prediction programs over most of their length are predicted by tRNAscan-SE (sean Eddy, are ness encoding tRNAs are predicted by tRNAscan-SE (sean Eddy, simple repeats are identified by repeatmasker (Arian Smit, http://genome.wustl.edu/edgy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RN/RepeatMasker.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(<3079. .3438,3582. .>4265))
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.4%;
Matches 2909; Conservative
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DNA linear PLN 10-JUN-1999
C-5 desaturase (STE1) gene,
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The Arabidopsis dwff/stel mutant is defective in the delta7 sterol C-5 desaturation step leading to brassinosteroid biosynthesis Plant Cell 11 (2), 207-221 (1999)
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                                                                                                                                            Arabidopsis thaliana
Bukaryota; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Beprantophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2294)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Arizona,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 2294)
Choe,S., Tanaka,A., Gregory,B.D. and Feldmann,K.A.
Choe,S., Tanaka,A., Gregory,B.D. and Feldmann,K.A.
Direct Submission
Submitted (66-NOV-1998) Plant Sciences, The University
Forbes Hall 303, Tucson, AZ 85721, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1300.8; DB 15; Lengt
Pred. No. 1e-233;
0; Mismatches 12; Indels
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/note="dwf7-2
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Direct Submission

Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the cranslation initiation start (ATG). A sequence are derived from the Ws or LAAR ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequences from Col-0. Genset carried out the library production and sequences from five full-length clones. Ceres, Inc. carried out the clustering of the full-length clones. Selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein id="Aam6060.1"
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/translation="MaadnaktimOVDETSFYNRIVLSHLLPANLMEPLPHFLQTWLR
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AANIHDCIHGANIWPVMGAGYHTIHHTTYKHNYGHYTIWMDWMFGSLRDPLLEEDDNKDS
FKKAE.
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2 (bases 1 to 1163)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
Full-Length cDNA from Arabidopsis thaliana
Unpublished
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Pred. No. 8.3e-77;
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/db_xref="taxon:3702"
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Brover, V., Troukhan, M.,
Feldmann, K.
Direct Submission
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Magnoliophyta; Eudicotyledons;
I (bases II) Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 1163)
Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Full.length messenger RNA sequences greatly improve genome annotation.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Unclassified.
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I (Dases I to 1175)

Karumanadas, B., Post-Beittenmiller, M., Venkatramesh, M.,
Kishore, G.M., Thorne, G.M. and LeDeaux, J.R.
Transgenic plants containing altered levels of steroid compounds
Patent: US 6822142-A 3 23 -WOV-2004;
Monsanto Company; St. Louis, MO
Location/Qualifiers
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                                                                                                           880 GTCTCTCTCAACCTTTCCAATTATATTGTTACAAACATTTGCTGTCTAGTTTAAAACATG
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Sequence 23 from patent
AR608874
AR608874.1 GI:56663610
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Best Local Similarity
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Submitted (16-58P-2004) Motoaki Seki, RIKEN Genomic Sciences Submitted (16-58P-2004) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:mseki@gsc.riken.jp, Yokohama, Kanagawa 145-503-958) Muklihttp://rarge.gsc.riken.jp/, Tel:81-45-503-9625, Pax:81-45-503-9586) An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This clone is in a modified pluescript vector.

Pleage visit our web site (http://rarge.gsc.riken.jp/) for further
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TVSESMIERGWTKCFASIGEFGWILYFVYIAIYLVFVEFGIYWMHRELHDIKPLYKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K., Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K., Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P., Ewaai,J., Hayashizaki,Y. and Shinozaki,K.
PLN 09-SEP-2004
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Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs Unpublished
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                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana mRNA for sterol-C5-desaturase, complete cds,
                                                                             GTCTCTCTCAACCTTTCCAATTATATTGTTACAAACATTTGCTGTCTAGTTTAAAACATG
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/organiam="Arabidopsis thaliana"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/gene="At3g02580"
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/gene="At3g02580"
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TWSESMIERGWTKGFFALGFGWILYFVYIAILYIVFYYIAILFIYPFHIGLLFWRAIWA
ANTHDCIHGNIWPVWGAGYYTIHHTTYKHNYGHYYIWMDWMFGSLRDPLLEEDDNKDS
FKKAE"
                                                                                                                                                                                                                                                                                  Gachotte, D., Husselstein, T., Bard, M., Lacroute, F. and Benveniste, P. Isolation and characterization of an Arabidopsis thaliana cDNA encoding a delta 7-sterol-C-5-desaturase by functional complementation of a defective yeast mutant plant J. 9 (3), 391-398 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-JUL-1995) D. Gachotte, Institut de Biologie
Moleculaire Plantes, Enzymologie Moleculaire et Cellulaire,
Institut de botanique 28, rue Goethe, F- 67083 Strasbourg, FRANCE
Location/Qualifiers
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larity 97.6%; Pred. No. 3.3e-76;
Conservative 0; Mismatches 10; Indels 2
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Brerol-C5-desaturase gene.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Direct Submission
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 421 28-FBB-2002;
The Scripps Research Institute (US); Syngenta Participations AG (CH)
                                                                                                               ATATGGACGGCGAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA
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Best Local Similarity 72.4%; Pred. No. 7.7e-55;
Matches 508; Conservative 0; Mismatches 108;

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/organism="Arabidopsis thaliana"

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Yamamoto, R. and Fukuda, H.
Direct Submission
Submitted (02-AUG-2005) Ryo Yamamoto, National Institute of Crop
Science (NICS); Kannondai 2-1-18, Tukuba, 305-8518, Japan
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GGVLLYFISGFLWCFYIYHLKRNVYIPKDALPSNKAMLLQISVAMKAMPWYCALPSLS
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HHIYNKQNTLSFPGALFHPLDGILQAVPHVVALLLVPWHSCTHIALIFLEALWTANI
HDCIHGKVFPVWGAGYHTIHHRTYRHNYGHYTIWMDWMFGTLRDPVEEDAKKM"
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National de la Recherche Scientifique, 28 rue Goethe, Strasbourg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2093 CTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAAATGTTACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2153 CACTIGACCATTICAACTGGTTCCTCTGTTTCCTCTACATAGCTCTCTATCTTGTTTTAG
                                                                                                                                                                                                                                                                                                                                                                              Husselstein, T., Schaller, H., Gachotte, D. and Benveniste, P. Delta7-sterol-C5-desaturase: molecular characterization and functional expression of wild-type and mutant alleles Plant Mol. Biol. 39 (5), 891-906 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ume type="calli derived from leaf protoplasts".918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product==sterol-CS(6)-desaturase"
/protein_id="AAD04034.1"
/db_xref==GI:4140398"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.8%; Score 228; DB 15;
61.1%; Pred. No. 1.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1155
/organism="Nicotiana tabacum"
                                                                                                                                                                                                                                                                     tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="xanthi SH6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db xref="taxon:4097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                GI:4140397
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                                                                                                                                                                                                                                                 /product="delta7 sterol C-5 desaturase"
/protein id="BAB16981.1"
/brotein id="BAB16981.1"
/dr xref="di:71934080"
/translation="MDDYLSLEVTETTWYNQIVLGTILLPEKLWTPLPHFLQTWLRNYI
AGTIVYLISGFLWCFYIYHLKRNVYVPKDA.PPTRAMYLQIYVAMKAMPWYCALRAVS
RYNDKNGWATRCFRISDVGMASYISYMTLYLIFEVEGIYWMRELHDIKPLYKWLHAT
HHINKQNTLSGFGALFHALDGILQAIPHYTALFLVFTHWTHILLLLEWBALWTANI
HDCIHGKFWPVMGAGYHTIHHTTYRHNYGHYTVWMDWMFGTLRDPLEEERAKNM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2271 GCATCTCCATGCTACCCATCATATGTACAAGCAAAACACACTCTCTCCATTTGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%; Score 228.2; DB 15; Length 1104; 60.9%; Pred. No. 1.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
   (E-mail:brassin@affrc.go.jp, Tel:81-29-838-8392)
Fax:81-29-838-8392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.5e-32;
0; Mismatches 198;
                                                         1. .1104
/organism="Zinnia elegans"
/mol_type="mRNA"
/db_xref="taxon:34245"
                                     Location/Qualifiers
                                                                                                                                                                              1. .816
/gene="ZeSTE1"
/note="STB1"
/codon_start=1
                                                                                                                                          l. .1104
/gene="ZeSTE1"
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Matches 443;
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/translation="MDDYLNLFIEETSFYNRVVLGTFLPESWWGPLPHWFQGWLRNYI
GGVLLYFISGFLWCFYIYRLKRNVYIPKDAIPSNRAWLQCYGWAKKAMPFYCALDSLS
EYNINWGWYKCFSRISDVGWLSYLIYMAVYLVIVEFGIYWMHRELHDIKLLYKYLHAT
HHIYNKQNTLSPFAGLAFPHDGILQAVPHVVALFLLPEHFTTHIALLFIEALWTANI
HDCKHAKVWPVMGAGYHTIHHTTYRHNYGHYTIWMDWMFGTLRDPVEDEVKKM"
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                                                                                                                                                                                                                                                                                                                    GCCATTTTATTGTGCTCTTCCGTCACTTTCTGAGTATATGATTGTAAATGGGTGGACAAA
                                                                                                                                                                                                                                                                                                                                                                                            462 AIGITICICAAGAATTAGCGACGTIGGATGGCTTICCTACCTIATTTATATGGCAGTTTA
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Pred. No. 8.4e-31;
0; Mismatches 172; Indels
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xref="GI:4426627"
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1 (bases 1 to 1447)
Famodu,0.0. and Rafalski,J.A.
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                                                                                    TGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGGTGACTTCTTTA 2392
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Nicotiana tabacum

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1148)

Husselstein,T., Schaller,H., Gachotte,D. and Benveniste,P.

Dolta7-sterol-C5-desaturase: molecular characterization and functional expression of wild-type and mutant alleles

Plant Mol. Biol. 39 (5), 891-906 (1999)
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                ATCTCCATGCTACCATCATATGTACAACAAGCAAAACACACTCTCTCCATTTGCCGGTA
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                                         569 ATCTCCATGCTACATATTTACAACAAGCAAAATACACTTTCCCCATTTGCTGGT
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/protein_id="AAD20458.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="xanthi SH6"
/db xref="texon:4097"
/cal_type="protoplast (calli)"
/tissue_type="leaf"
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                                                                                                            Length 1447;
                            DE;
Sterol metabolism enzymes
Patent: US 6465717-A 27 15-OCT-2002;
B. I. du Pont de Nemours and Company; Wilmington,
EPX;
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Unclassified.
1 (bases 1 to 1210)
Famodu,O.O. and Rafalski,J.A.
Sterol metabolism enzymes
Patent: US 6465717-A 29 15-OCT-2002;
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US 6465717.
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/organism="unknown"
/mol_type="genomic DNA"
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1. .1447
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Sequence 29 from patent
AR237881
AR237881.1 GI:27282714
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Matches 399; Conserv
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Triticum aestivum clone wrl.pk0107.a5:fis, full insert mRNA
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Trificum aestivum (bread wheat)

Trificum aestivum (bread wheat)

Trificum aestivum (bread wheat)

Trificum aestivum (bread wheat)

Trificum aestivum

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooladeae; Trificaea; Trificum.

1 (bases 1 to 1210)

Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,

Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
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                                                                                                                                                             Length 1210;
                                                                                                                                                    6.4%; Score 100,
59.8%; Pred. No. 4.9e-25;
rive 0; Mismatches 175; Indels

    1210
    organism="unknown"
    mol_type="genomic DNA"

Location/Qualifiers
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BT009523.1 GI:32129074
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Matches 389; Conservative
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Direct Submission
Submitted (20-UUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
                                                                                                                                                                                                                                                                                                                                          188 AGATGCTCTCCTACAGTAGAAGCTATGAAGAAGCAATAATTGTTGCATCAAAGGCTAT 247
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Best Local Similarity 59.8%; Pred. No. 4.9e-25;
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps
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ADX49989
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ABX72194
ADX11411
ABX191992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK89916 standard; DNA; 2925 BP.
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                                                                                                                                                                                                                                                                              and encoding polymuclectides that impart at least one dwf7 mutant phenotype when expressed in a plant. The polymucleotide sequences conciding the mutant dwf7 proteins are useful for producing transgenic plants from transformed plant calls. The polymucleotide sequences are useful for altering the sterol composition of a plant relative to the wild-type plant. The transgenic plant has less cholesterol or increased atealor production relative to the wild-type plant. The mutant sequences are also useful for isolating or creating other mutant call gene alleles and for detecting plant regulatory defects which can affect plant growth. The present sequence encodes Arabidopsis thaliana dwf7 homologue protein,
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                                                                                                                                                                                                                                                                   present invention relates to the isolation of dwarf7 (dwf7) mutants
                                                                                                                                                 Novel isolated dwf7 polynucleotide for altering sterol composition of a plant, by introducing polynucleotide into plant cell to produce transformed plant cell and producing transgenic plant from transformed
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Best Local Similarity
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(ARIZ-) ARIZONA BOARD OF REGENTS
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1740 1800 1860 1440 1620 1680 TAGTAAACGCAATTTAACCCTTATAAGTTTAATCGTATTCAACGAATGACCCAGAGACTT ACAACCGAATGGTTCTGAGTCACCTTTTGCCGGTGAATCTATGGGAACCTTTACCACATT TCCTCTGGGGCTTCTACATCTATACCTTAAACTCCAACGTTTACGTCCCCAAAGGTTACT TICTACTICTCATTTAATTAGTTTTAAAGTTTAATATTTTTGGCTAATCCACATTTTTA AGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTGAAATTTGTGGTTC AAGACTCCATTTTTGTTTAAGGTAAACCTTGAATCTCATAGATTGTCGATTGTTGGTATT TCCATTITCAGGTACGGTTCTGTAGACTGTAGTCTTGCTGACCAGTCCGGCTTAACCACC GITAATCCGTCTAGCTTTACTCTTTAGACCTACCTTAGACAGTTAGACACCTGCTAATTA ATGAGTTTCCTTTTCTTGTTCAGCAAGTTACCTGTGTTACTTGAGAGTTGAGTTAATGG 1321 TARATARATCCATCGTARCCTCCACTTCARATTCTTTTTARARAGTRGCARTCATTT GGCCATATCTCTCTCTAACAAACGCATAGTAACACTTGACCACAGTTTGACTTCTCGGCG GITICATGGCGGCGACIATGGCAGATTATAATGATCAGATCGTCAATGAGACCTCTTTTT ACAACCGAATGGTTCTGAGTCACCTTTTGCCGGTGAATCTATGGGAACCTTTACCACATT TCCTCCAGACATGGCTCCGGAACTACCTCGCCGGAAACATACTCTTCATCTCCGGCT TTCTACTTCTCATTTAATTAGTTTTAAAGTTTAATATTTTTGGCTAATCCACATTTTTTA GTTAATCCGTCTAGCTTTACTCTTTAGACCTAGCTTAGACAGTTAGACACTGCTAATTA TAGTAAACGCAATTTAACCCTTATAAGTTTAATCGTATTCAACGAATGACCCAGAGACTT AAATATTGTAAGTTTGCTTCGTAAATTGTAGCTACAGATCTCAAAGCTCCTCCTGTT TCCTCTGGTGCTTCTACATCTATTACCTTAAACTCAACGTTTACGTCCCCCAAAGGTTACT GCCTGATAGATTGTGTTATACGTTAACCTTTTTTTTTCTTACTGTTACTTTTCAGTTCTTGTC

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                                      TTAGTTCTATTTCTTGCTTGGTTTCTTCTATTTTTTGTGGGTTAGAATCCATTCCTACGAGA
                                                                                         AAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTATGCCTTGGTACACTCTTCTT
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The present invention relates to the isolation of dwarf? (dwf?) mutants and encoding polymucleotides that impart at least one dwf? mutant phenotype when expressed in a plant. The polymucleotide sequences encoding the mutant dwf? proteins are useful for producing transgenic plants from transformed plant cells. The polymucleotide sequences are useful for altering the sterol composition of a plant relative to the wild-type plant. The transgenic plant has less cholesterol or increased sterol production relative to the wild-type plant. The mutant sequences are also useful for isolating or creating other mutant cell gene alleles, and for detecting plant requiatory defects which can affect plant growth. The present sequence encodes Arabidopsis thaliana dwf? protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated dwf7 polynucleotide for altering sterol composition of a plant, by introducing polynucleotide into plant cell to produce transformed plant cell and producing transgenic plant from transformed
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Gene encoding Arabidopsis thaliana dwf7 protein.
                                               Dwarf7; dwf7; plant cell; sterol composition;
plant regulatory defect; plant growth; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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31.6%;
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FELDMANN K A.
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P-PSDB; AAU99577.
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The invention relates to an isolated dwarf7 (dwf7) polynucleotide that imparts at least one dwf7 mutant phenotype when expressed in a plant. The invention also relates to a recombinant vector comprising the dwf7 polynucleotide and control elements that are operably linked to the polynucleotide and control elements that are operably linked to the colon polynucleotide and control elements is netrologous to the coding sequence, a nost call transformed with the recombinant vector above, a method of producing a transgenic plant comprising the polynucleotide, a cransgenic plant comprising the polynucleotide, a polynucleotide at a transgenic plant relative to the wild-type plant. The dwf7 polynucleotides and polypeptides are useful for producing transgenic plants have altered structure or morphology. The transgenic plants are useful in plant breeding, in agricultural production or in industrial applications. The dwf7 polynucleotides are useful for resoluting other mutant alleles and for enhancing certain features such a supplications. The dwf7 polynucleotides are useful for conferring and increased seed production. They are also useful for conferring desired creating other mutant alleles and for enhancing certain features such a increased seed production. They are also useful for conferring desired craits on any plant, for altering sterol composition of a plant thus conferring the biosynthesis of brassinosteroids. The dwf7 control element is useful as a plant promoter to express any protein of interest in a transgenic plant, particularly to express a protein involved in cransgenic plant, particularly to express a protein involved in brassinosteroid biosynthesis. The DWF7 polypeptide is useful in any confidention of plant structures and experimental or industrial applications, e.g., regulation of sequence represents thale cress confidential applications of plant structures and experimental confidential plant has a plant thus expensed by a protein of plant element confidential elements. This sequence represents thale cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated dwarf 7 (dwf?) polynucleotide, useful for conferring desired traits on essentially any plant and for altering sterol composition of a plant thus increasing or reducing cholesterol content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCATGCCACCCATCATATCTACAAGCAGAATACACTCTCTCCCATTTGCCGGTAAGTG 120
                                             Thale cress, dwarf7; dwf7; sterol; plant breeding; fruit production; agricultural production; flowering; leaf production; frout production; branching; seed production; cholesterol; brassinosteroid;
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              cress dwarf7 (dwf7) DNA
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99.6%;
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Matches 958; Conservative
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                                                                                                                                    Arabidopsis thaliana
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P-PSDB; ADQ28842.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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31-AUG 7-58P-11 13-58P-11 14-58P-11 15-58P-11 15-58P-11 15-58P-11 15-58P-11 15-58P-11 15-58P-11 15-58P-11 16-58P-11 17-60T-11 17-6	Query Match Best Local Matches 48	462	521	732	580	4 (	700	912
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The invention describes a plant (I) comprising DNA encoding a polypeptide (PI) with 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity and a polypeptide (P2) with steroid pathway enzyme activity such as gualene epoxidase, sterol methyl transferase I, sterol C4-demethylase, btusifoliol C14alpha-demethylase, sterol C5-desaturase or sterol methyl transferase I in naryme activity, in its genome. A recombinant vector transferase II naryme activity, in its genome. A recombinant vector repressing P1 is useful for increasing the formation of steroid pathway products in a transformed host cell as compared to an otherwise identical north a vector expressing P1 or P2 (III), or a transgenic plant produced with a vector expressing P1 or P2 (III), or a transformed by secondinant vector (II) is useful for producing a plant by sexually crossing (I), (II) or (III) with a non-transformed plant. A cholesterol lowering composition (IV) containing (V), and a pharmaceutical pathway product (V), a food product containing (V), and a pharmaceutical composition containing (V) is useful for lowering the plasma
                                                                                               1001
GTCTCTCTCAACCTTTCCAATTATATTGTTACAAACATTTGCTGTCTTAGTTTAAAACATG 1151
                                                           879
                                                                                                                                     939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Squalene epoxidase; antilipemic; steroid pathway enzyme activity; 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme; squalene epoxidase; sterol methyl transferase I; sterol C4-demethylase; obtusifoliol C14alpha-demethylase; sterol C5-desaturase; sterol methyl transferase II; cholesterol lowering composition;
                                                                                                                                     GTCTCTCTCAACCTTTCCAATTATATTGTTACAAACATTTGCTGTTTAAAACATG
                                                                             GTIGTIGTICAAAGTTTCAGCCTTTCTTGTTCTTTTTCTTCTTCTTCTTTTTTATG
                                                         GITGITGITGAAAGITICAGCCITICITGITCITITITCITCITCITCITATICATGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New transgenic plant containing altered levels of steroid compounds useful for producing oil which is useful for making a composition for treating elevated plasma concentration of low density lipoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis sterol C5-desaturase polynucleotide.
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                                                                                                                                                                                                                                                                                                                                             ABS53044 standard; DNA; 1175 BP
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concentration of low density lipoprotein cholesterol or for treating or preventing an elevated plasma concentration of low density lipoprotein cholesterol. (1), or a transgenic plant is useful for making a food additive composition by obtaining oil containing a steroid pathway product from seed of (1), or a transgenic plant and mixing the oil with an edible solublising agent, a dispersant, and optionally an antioxidant. (V) is useful for reducing the concentration of low density lipoprotein cholesterol in plasma. (1) has improved nutritional characteristics. This sequence represents an Arabidopsis thaliana sterol C5-desaturase
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                                                                                                                                                                                                                                                                           TTTACAGGGCTTGCA-TTCACCCAGTAGACGGGATACTTAAGGCTGTACCGCATGTGATA
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                                                                                                                                                                                                            Length 1175;
                                                                                                                                                                              Sequence 1175 BP; 300 A; 265 C; 227 G; 383 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana; plant; gene; stress; transgenic; ds
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                                                                                                                                                                                                                                           10; Indels
                                                                                                                                                                                                             ; DB 6;
1.5e-97;
                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                            Score 461;
Pred. No. 1
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                                                                                                                                                                                                          Query Match 15.8%;
Best Local Similarity 97.6%;
Matches 489; Conservative
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                                                                                                                                              polynucleotide
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2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTAT
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                                                                                                         739 CATAACTATGGTCATTATACCATATGGATGGATTGGATGTTTGGCTCTCTTAGGGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding sterol metabolism enzyme useful for producing transgenic plant, has nucleotide sequence encoding the polypeptide having sterol delta-7 reductase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corn; wheat; rice; soybean; plant; gene; ss; sterol metabolism;
sterol delta 7; reductase; sterol C5 desaturase.
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Pred. No. 3.4e-37;
0; Mismatches 166; Indels 86;
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                                                                                                                                                2682 TTAGCAGAAAAGACAGTTTCAAGGAGAAAAGTGAGAA 2723
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                                                                    2622 CATAACTATGGTCATTATACCATATGGATGGACTGGATGTT
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Matches 399; Conservative
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                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to ablotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTGTTTTAGTTTATGATTTATTGGGTTCACAAAGAGCTTCATGACATTAAATT 2261
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                                                                                                                                                                                                                                                          Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCATGGTACACTCTTCTTCCAACTGTCTCCGAGAGTATGATTGAACGTGGTTGGACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCATAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%; Score 347.2; DB 6; Length 846; 72.4%; Pred. No. 6e-71; Live 0; Mismatches 108; Indels 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 846;
                                                                                                                                                                                                                                                                                                                           Claim 144; SEQ ID NO 421; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 846 BP; 222 A; 198 C; 170 G; 256 T; 0 U; 0 Other;
                                                                                                               ) SCRIPPS RES INST.
) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                           Wang X,
                          24-AUG-2000; 2000US-027866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                           Kreps J,
                                                                                                                                                                                                                  WPI; 2002-304127/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 508; Conserv
                                                                                                                                                                             Harper JF,
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2202 TCTTGTTTTAGTTGAGTTTATGATTTATTGGGTTCACAAGAGCTTCATGACATTAAATT 2261
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                                                                                                           New polynucleotide encoding a transcription factor polypeptide, useful in genetic mapping for plant breeding.
                                                                                                                                                                                         The invention relates to a polynucleotide which encodes a transcription factor. The nucleic acid fragment is useful in genetic mapping for plant breeding. The present sequence is sterol-C5-desaturase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        556 GCTTTACAAATATCTTCATGCTACCCATCACATCTACAATAAAACAGAACACTCTCTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       629 ------GCATTTCACCCTCTTGATGGG
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                                                                                                                                                                                                                                                                                       Query Match 7.0%; Score 203.4; DB 12; Length 1447; Best Local Similarity 61.3%; Pred. No. 3.4e-37; Matches 399; Conservative 0; Mismatches 166; Indels 86;
                                                                                                                                                                                                                                                           Sequence 1447 BP; 444 A; 283 C; 294 G; 426 T; 0 U; 0 Other;
                                 Shen JB;
                                 Rafalski JA,
                                                                                                                                                             Claim 2; SEQ ID NO 27; 43pp; English.
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                                 Ĕ,
                                                               WPI; 2004-052051/05
                                 Orozco
   (SHEN/) SHEN J B.
                                                                              P-PSDB; ADI19007
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TCTTGTTTTAGTTGAGTTTTATTGGGTTCACAAAGAGCTTCATGACATTAAATT
                                                                                                              2382 TGACTTCTTTACTTGATGTTTTTCGGGTTTTCAGGGCTCGCATTCCATCCGCTGGACGGG
                                                                                                                                                                                                                                                                                                                  ------GCATTTCACCCTCTTGATGGG
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                                                                                                                                                           2142 ATGITACICTACACTIGACCATTICAACTGGTTCCTCTGTTTCCTCTACATAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription factor; genetic mapping; plant breeding; sterol-C5-desaturase; soybean; gene; ss.
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/*tag= a
/product= "Sterol-C5-desaturase"
/partial
/note= "No start codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                         629 -----
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(OROZ/) OROZCO E M.
(RAFA/) RAFALSKI J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003229914-A1
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19-NOV-1999;
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P-PSDB; ADI45357
                           US2004010815-A1.
                  haeme; yield
                       Oryza sativa
                                       26-SEP-2001;
04-APR-2002;
                                            04-APR-2002;
                               15-JAN-2004
                                                                           Lange BM,
Goff SA,
                                                                 (MOUG/)
(PROV/)
(RICK/)
                                                        (GLAZ/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a polynucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide encoding a polypeptide comprising an authoridise and sequence convoluted in or associated with the biosynthesis of isoprenoids in a plant, an expression cassette comprising the polympetide, a host cell comprising the polympetide and transgenic plant comprising the expression cassette. The polypeptide and polymucleotide, a host cell comprising the expression cassette. The polypeptides and polymucleotides include those associated with the biosynthesis of isopentenyl diphosphate (IPP) and dimethylallyl alcohol (DMAPP), the biosynthesis of short-chain plastid alcohol (DMAPP), the biosynthesis of short-chain plastid carotenoids and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or phyloquinone biosynthesis of tocopherols, plastoquinone and/or phyloquinone biosynthesis of ubiquinone, biosynthesis of ubiquinone, biosynthesis of ubiquinone, biosynthesis of ubiquinone, biosynthesis of chlorophyll or haeme. Also disclosed are banana, wheat and corn homologues of some of the rice polymucleotides. The corn homologues of some of the rice polymucleotides are useful for producing transgenic plants, where the genome is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g. to result in a loss, a decrease or an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce a better quality product than the corresponding wild-type plant. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.
                                                                                       Rice, isoprenoid biosynthesis, 88, gene; plant; isopentenyl diphosphate; IPP; dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone; phylloquinone; mevalonate pathway; phytosterol; brassinosteroid; ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll;
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Moughamer T, Provart N, Ricke
                                              Rice isoprenoid biosynthesis-associated cDNA #144
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Katagiri F, Kreps J,
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2002US-0370743P
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  (first entry)
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COOPER B.
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KREPS J.
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RICKE D.
ZHU T.
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                                                                                                               segdata.uspto.gov/seguence.html?DocID=20040010815. The present seguence is a Rice isoprenoid blosynthesis- associated cDNA of the invention.
                           as markers and probes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            631 ACATTGCTCTTCTTCATAGAGGCCGTGTGGACAACTAACATCCATGACTGCATTCACG
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acid molecules are useful for targeted gene disruption, as use and probes. Note: The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                     79;
                                                                                                                                                                                                                                                            DB 12; Length 833;
                                                                                                                                                                                                   Sequence 833 BP; 199 A; 226 C; 193 G; 215 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                     0; Mismatches 191; Indels
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                                                                                                                                                                                                                                                            Score 189.4; DB 1;
Pred. No. 5.3e-34;
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                                                                                    format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                           393; Conservative
                                                                                                                                                                                                                                                                                          Best Local Similarity
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The invention relates to a polymucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide encoding a polypeptide comprising a maino acid sequence encoding a polypeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isoprenoids in a plant, an expression cassette comprising the polymucleotide, a host cell comprising the cassette comprising the polypeptides and polymorleotide, a host cell comprising the cassette. The polypeptides and polymucleotide include those associated with the biosynthesis of isopententyl diphosphate (IPP) and dimethylallyl alcohol (DWAPP), the biosynthesis of short-chain plastid presylutransferases, the biosynthesis of gibberallins, the biosynthesis of presylutransferases, the biosynthesis of dibosynthesis of tocopherols, plastoquinone and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or phylloquinone biosynthesis of tocopherols, plastoquinone and/or phylloquinone biosynthesis of colorophyll or haeme. Also disclosed are banana, wheat and corn homologues of some of the rice polymucleotides. The plants may also materials of the rice polymucleotides. The plants may also have increased yields and/or produce a lost of the print the corresponding gene has been disrupted, e.g. to result in a loss, and alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce and lectrase or an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce are useful for trageted gene disruption, as well as markers and probes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence is a wheat isopremoid biosynthesis-easeclated cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.
dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase;
glbberellin; caroctenoid; abscisic acid; tocopherol; plastoquinone;
phylloquinone; mevalonate pathway; phytosterol; brassinosteroid;
ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll;
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rovart N, Ricke D;
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Katagiri F, Kreps J, Moughamer T, Provart N,
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04-APR-2002; 2002US-0370620P.
04-APR-2002; 2002US-0370743P.
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MOUGHAMER T.
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Goff SA,
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                                                                                                                                              GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA
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                                                                                                               AGATGCTGTCCCTACAGTAGAAGCTATGAAGAAGCAAATAATTGTTGCATCAAAGGCTAT
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                           Length 1135;
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Sequence 1135 BP; 243 A; 292 C; 296 G; 304 T; 0 U; 0 Other;
                                                       Indels
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                                                        175;
                           12;
                                          1.2e-33;
                           B
                                            Pred. No. 1.2e
0; Mismatches
                           Score 188;
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                                         59.88;
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                                         Best Local Similarity 59.8
Matches 389; Conservative
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                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide encoding a transcription factor polypeptide, useful in genetic mapping for plant breeding.
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                       CATAACTATGGTCATTATACCATATGGATGGACTGGATGTTTGGCTCTCT
                                                     Sequence 1210 BP; 323 A; 288 C; 293 G; 305 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 6.4%; Score 188; DB 12; Length 12
1 Similarity 59.8%; Pred. No. 1.3e-33;
389; Conservative 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription factor; genetic mapping; plant breeding; sterol-C5-desaturase; wheat; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Sterol-C5-desaturase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "No start and stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           Wheat sterol-C5-desaturase cDNA #2
                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                        ADI19008 standard; cDNA; 1210
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(OROZ/) OROZCO E M.
(RAFA/) RAFALSKI J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-052051/05.
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19-NOV-1999;
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0; Mismatches 175;
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                                                     DUPO ) DU PONT DE NEMOURS & CO E I.
98US-0109283P
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                                                                                                                                                                     WPI; 2003-147075/14.
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20-NOV-1998;
                                                                                                                Famodu 00,
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Transcription factor; genetic mapping; sterol-C5-desaturase; corn; gene; ss.
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Matches 388; Conservative
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                                                                                                                                                                           ATACTGCAAGCCATATCGCACGTGATTGCTCTTCTCCCGATGCACTTCAGGACG
                         rcrcarcrirergagerreggarriracregarecacagagagrrecareacaraaagec
                                                                                 ATTIGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGG
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                                                                                                                                                                                                                                                                             CATAACTATGGTCATTATACCATATGGATGGACTGGATGTTTGGCTCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                        Corn; wheat; rice; soybean; plant; gene; ss; sterol sterol delta 7; reductase; sterol C5 desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding corn sterol C5 desaturase protein #2
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                                                                                                                                                                                                                                                                                                                                               ABX15832 standard; cDNA; 911
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P-PSDB; ABG73988
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Bequences may also be useful for producing a transgenic plant, by transforming a plant cell with the CDNA sequence and regenerating a transgenic plant from the transformed plant cell. The nucleotide sequence is useful for obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding a sterol delta-7 reductase or a sterol-C5 desaturase polypeptide. Probes derived from the nucleotide sequence of the invention may be useful for physical mapping. The present sequence represents a cDNA sequence encoding a sterol metabolism enzyme of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 GCAAGGTATGGCCAGTCATGGGCGCTGGGTATCACACCATCCACCATACGACTTACCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 187; DB 8; Length 911;
Pred. No. 2e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 175; Indels
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                                                                                                                                                                                                                                                                                                                                                                           polynucleotide encoding a transcription factor polypeptide, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTITITACTGTGCTCTTCCAACTITATCTGAGTATATGATCGAGAGTGGATGGACCGG 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a polynucleotide which encodes a transcription factor. The nucleic acid fragment is useful in genetic mapping for plant breeding. The present sequence is sterol-C5-desaturase cDNA.
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Best Local Similarity 59.8%; Pred. No. 2e-33;
Matches 388; Conservative 0; Mismatches 175; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 911 BP; 222 A; 214 C; 217 G; 258 T; 0 U; 0 Other;
                                                            /*tag= a
/product= "Sterol-C5-desaturase"
/partial
/note= "No start and stop codon"
                                                                                                                                                                                                                                                                                                            Shen JB;
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                                   Location/Qualifiers 74. .646
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                                                                                                                                                                             21-AUG-2002; 2002US-00224880
                                                                                                                                                                                                       98US-0109283P.
99US-00443041.
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OROZCO E M.
RAFALSKI J A.
SHEN J B.
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P-PSDB; ADI19003.
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19-NOV-1999;
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2503 ATCTGAGTCTTTTGGTAGGGATATGGACAGCAAGCATCCATGATTGCATACATG 2562
408 TTCTGCAAGCAATACCGCATGTGCTTTGCTCTCCTCCTCCCAACGCACTTCAGGACGC 467
                                                                                                                                                                                  2623 ATAACTATGGTCATTATACCATATGGATGGACTGGATGTTTGGCTCTCT 2671
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Job time : 1588 secs
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score:

Title: Perfect

Sequence:

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Run on:

Scoring table:

Searched:

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Minimum | Maximum |

Database

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CL957247 OSIFCC000
CX099651 RECM0308
DR109676 RTS1 4 A0
CF227924 PEAXMO06
CK251357 RST734994
CN884525 010811AAS
CD938892 OV.111G01
BW685027 BW685027
CX659607 PO01032G0
CN493842 Mdfw2007d
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                   DRS64230 WS0335.C2
DR069207 RTALL 7
ECB240394 PopSC037
CCN130796 RHOHL 43
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CD44877 EL0100329
CA252633 SCVPFL114
DR469736 WS00948.B
CP272845 EST13618
DR934643 EST13618
DR934643 EST13618
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WS00753.C
WS0335.C2
RTAL1 7 E
PopSC0037
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 940)
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3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Bmail: allen.sessions@syngenta.com
ABRC Stock Number CS841870, T-DNA left border flanking sequences o
Syngenta Arabidopsis Insertion Library (SAIL) lines are available strongh the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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/clone="SAIL 1124 H08.v1"
/clone="Ib="SAIL Collection"
/note="T--DNA left border sequences were isolated using a
modified TAIL-PCR strategy"
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/mol_type="genomic DNA"
/ecotype="Columbia"
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Arabidopsis thaliana
  DRS 80137
DRS 84230
DRS 84230
DRS 92230
CR240394
CR2436598
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SOURCE
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BH956101 odg94D06.
CE8255600 16-E01842
CL488421 SAIL 508
CD822918 BN25.0478-
BZ384971 SALK 1362
CD82327 BN25.048G
CD82327 BN25.048G
CK264500 EST710578
CK264500 EST710578
CK264500 EST710577
CK264990 EST710577
CK264990 EST710577
CK31853 24KDBNH U
CC877047 RA SEAOOO
CC87704 FA SEAOOO
CC87704 FA SEAOOO
CC87704 SET112385
DR942311 EST112385
CK979536 CAB40007-
BK687757 BW687757
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CD834215 BN45.040P
CL516186 SAIL_914_
                                                                                                                                                           7, 2006, 09:09:41 ; Search time 11150 Seconds (without alignments) 12273.741 Million cell updates/sec
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Biocceleration Ltd.
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                        GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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gb_est2::;

gb_est4::;

gb_est5::;

gb_est7::;

gb_est7::;

gb_gss2::;

gb_gss2::;
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Contact: Sessions A
Applied Trait Generics
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Bmail: allen.sessions@syngenta.com
ABRC Stock Number CS841192; T.DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
class: TDNA tagged.
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SAIL 914 D07.v2 SAIL Collection Arabidopsis thaliana genomic clone SAIL 914 D07.v2, genomic survey sequence.
CL516186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

    (Dases 1 to 963)

357 ATGTTACTCTACACTTGACCAATTCAACTGGTTCCTCTGTTTTTGTTTACATCGTGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               571 ATACTTCAGGCTGCACCACATGTGATAGCTCTGTTCATAGTGCCGGTTCATCATAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGTTTTAGTTGAGTTTATGATTTATTGGGTTCACAAAGAGCTTCATGACATTAAATT
                                                                                                                                                               2442 ATACTICAGGCIATACCGCACGIGATAGCGCTGTITATAGTGCCGATTCATCATAACA
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                                                                                                                                                                                                                                                                                                                                                                                   2382 TGACTICITIACTIGATGTTTTTCGGGTTTTCAGGGCTCGCATTCCATCCGCTGGACGGG
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Arabidopsis thaliana
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BN45.040Pl3F011019 BN45 Brassica napus CDNA clone BN45040Pl3, mRNA
CD634215
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                                                                                                                                                                                                                            TTGGCCATATCTCTCTAACAAACGCATAGTAACACTTGACCACAGTTTGACTTCTCGG 1498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoplante.

Genoplante.

Unpublished (2003)

Contact: Genoplante

Genoplante

Genoplante

Genoplante

Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

761: 33 1 69 47 54 10

761: 33 1 69 47 54 10

7718 sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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llarity 75.7%; Pred. No. 9.3e-66;
Conservative 0; Mismatches 65; Indels
                             Indels
                                                                  1319 TTTAAATAAATCCATCGTAACCCTCCACTTCAAAATTCTT
      Pred. No. 3.5e-70;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/tissue type="seed"
/clone_Ibe="BN45"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD834215.1 GI:32516155
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Brassica napus
          Best Local Similarity 99.7
Matches 356; Conservative
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Best Local Similarity
Matches 471; Conserv
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Enterporta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases I to 700)

I (bases I to 700)

IS Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Mosh, W., Rabinowicz, P.D. and Wilson, R.K.

Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg94 row: b column: 06
Seq primer: -28RPpOT reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH956101 700 bp DNA linear GSS 01-OCT-2002 odg94b06.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
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                                                                                       /db xref="cxxx0:3702"
/clone="SALK 00869.45.50.x"
/clone="lb="Arabidopsis thaliana TDNA insertion lines"
/clone="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AAAACATGTAAATGTTTGATGATCTTTGCAAGACTCCATTTTTTGTTTAAGGTAAACCTTG 120
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                                                                                                                                                                                                                                                                                                                                                                    Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                 /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecoType="Col-0"
                                                                                                                                                                                                                                                                                                                                                               Query Match 10.2%; Score 299.4; DB 9 Best Local Similarity 96.4%; Pred. No. 1.9e-57; Matches 317; Conservative 0; Mismatches 11.
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High quality sequence stop: 551.
Location/Qualiflers
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BH956101.1 GI:23437328
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1 (bases I to 328)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., A Sequence-Indexan,J. and Ecker,J.R.
A Sequence-Indexad Library of Insertion Mutations in the Unpublished (2001)
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/clone lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALK 008569.45.50.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_008569.45.50.x, genomic
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                                                                                                                                                                                                                                                                   Length 963;
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                                                                                                                                                                                                                                                                Query Match 11.0%; Score 321; DB 10; Best Local Similarity 100.0%; Pred. No. 2.6e-62; Matches 321; Conservative 0; Mismatches 0;
                       organism="Arabidopsis thaliana"
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                                              /mol_type="genomic_DNA"
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SALL 508 H08.vl SAIL Collection Arabidopsis thaliana genomic clone CA488421
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/clone_lib="MplZ-ADIS-019"
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Salte_2: Sall primer adapter; RNA from cellculture (At7) 5
stee_2: Sall primer adapter incollation treated with 0.002 mM cycloheximid
for 2 h in the dark. Sequence submission managed by
RISDP(ABLI-Primary database: http://gabi.rzpd.de. This
for further information."
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Spermacophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[ bases 1 to 1016]
Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D.,
Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B.,
Mitzel, T., Kataglir, F., Glazebrook, J., Law, M. and Goff, S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
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/clone="MPIZD768G108Q"
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Plate: 8 row: G column: 10
Seg primer: T7R; CTAATACGACTCACTATAGGGA.
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Exi.

Arabidopsis thaliana

Eukaryora, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Eukaryora, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

II (bases I to 326)

Arabidopsis thaliana cDNA library enriched in transcription factors Arabidopsis thaliana cDNA library enriched in transcription factors

Ontact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planter institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaa@mpiz-koeln.mpg.de
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326 bp mRNA linear EST 31-DEC-2004
S-ED18428-019-008-G10-T7R MPIZ-ADIS-019 Arabidopais thaliana cDNA
clone MPIZp766G108Q 5-PRIME, mRNA sequence.
CB255600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATACCATATGGATGGACTGGATGTTTGGCTCTTTATGGTTCCTTTAGCAGAAAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 ATTATGGAAGGGATATGGACAGTGAGCAACCATGATTGCATCAATGGTAACATATGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2577 ATAATGGGTGCAGGATACCATACCATACACATACAACATACAAGCATAACTATGGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%; Score 285.6; DB 9;
83.0%; Pred. No. 3.1e-54;
iive 0; Mismatches 64;
       organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                      Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2809 AACATGACTGCATAATTTGA 2828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 365; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2457
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ORGANISM
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VERSION
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AUTHORS
TITLE
JOURNAL
COMMENT
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BZ384971 327 bp DNA linear GSS 26-NOV-2002 SALK 136266.46.25.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_136266.46.25.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTCTATCTTGTTTTAG 2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosida II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2273 ATCTCCAIGCTACCCATCATATGTACAACAAACAAACACTCTCTCCCATTTGCCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 TCTGGTGCTTCTATATCTATTACCTTAAGCTCAACGTTTACTTCCCCAAAGATTCAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACAAAAAAGGGGATGATTATGCAAATACATGTGGCAATGAAGGCTATGCCTTGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAAATGTTACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2333 TGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGGTGACTTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------GGGCTCGCGTTCCATCCTTTGGACGGGATACTTCAGGC
                                                                                                                                                                                                                                                                                                                                                  TGTGGTTCTTAGTTCTTGTTTGCTTGGTTTCTTCTATTTTTGTGTTTAGAATCCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTATGCCTTGGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2393 CTTGATGTTTTTCGGGTTTTCAGGGCTCGCATTCCATCCGCTGGACGGGATACTTCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2453 TATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCATAACACATCTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                                                                                                                                                                                                                                                          Length 749;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                          Score 281.6; DB 6;
Pred. No. 2.6e-53;
0; Mismatches 69;
and http://genoplante-info.infobiogen.fr)
Location/Qualifiers
1. .749
/organism="Brassica napus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGGITITIGGGAAGGGATATGGACAGCGAGCATC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                  /mol_type="mRNA"
/cultivar="lot Neuf"
/db_xref="taxon:3708"
/clone="BN25047B03"
/tissue_type="seed"
/clone_lib="BN25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BZ384971.1 GI:25483046
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                                                                                                                                                                                                                                                                              Best Local Similarity 73.0
Matches 419; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
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KEYWORDS
SOURCE
ORGANISM
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BZ384971/c
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                 Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Bmail: Blon. Research Triangle Park, NC 27709, USA
Bmail: allen. sessions@syngenta.com
ABRC Stock Number CS821429, T.DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1378 TTTAAATATTGTAAGTTTGCTTCATTCGAAATTGTAGCTACAGATCTCAAAGCTCCTCCT 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1558 TITACAACCGAATGGITCTGAGTCACCTITTGCCGGTGAATCTATGGGGAACCTITACCAC 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD822918 10-JUL-2003
BN25.047B03F020109 BN25 Brassica napus CDNA clone BN25047B03, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1438 GTTGGCCATATCTCTCTCTAACAAACGCATAGTAACACTTGACCACAGTTTGACTTCTCG 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 GCGGTTTCATGGCGGCGACTATGGCAGATTATAAATGATCAGATCGTCAATGAAGACCTCTT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 749)
Genoplante.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 TTTACAACCGAATGGTTCTGAGTCACCTTTTGCCGGTGAATCTATGGGAACCTTTACCAC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1618 ATTICCICCAGACATGGCTCCGGAACTACCICGCGGAAACATACTCTACTICATCTC 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 ATTICCTCCAGACATGGCTCCGGAACTACCTCGCCGGAAACATACTCTACTTCATCTAC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                     /mol type="genomic DNA"
/mol type="Columbia"
/db xref="taxon:3702"
/clone="SAIL 508 H08.vl"
/clone lib="SAIL 508 Lollection"
/note="T-DNA left border sequences were isolated using modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 283.8; DB 10;
Pred. No. 8.5e-54;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                     'organism="Arabidopsis thaliana"
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CD822918
CD822918.1 GI:32504858
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                                                                                                                                                                                                                                                                              1. .1016
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296; Conservative
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CD822918
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CD834242
BN45.041B07F011207 BN45 Brassica napus CDNA clone BN45041B07, mRNA
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                                    93, The Henri Rochefort 91025 EVRY CEDEX France

7el: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (http://www.genoplante.com

and http://genoplante-info.infoblogen.fr).
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Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 TGGATTGGATGTTTGGCTCTCTTAAAGACCCTCTTTTAGAAGATGTTGACAACAACAAGACA
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                                                                                                                                                                                                                /organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="RNS5048614"
/tissue_type="seed"
/clone_lib="BN25"
                                                                                                                                                                                                                                                                                                                                                                                                               Score 265.4; L
Pred. No. 1.2e-
0; Mismatches
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CD834242.1 GI:32516182
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Best Local Similarity 84.5%;
Matches 310; Conservative
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Brassica napus
  Contact: Genoplante
Genoplante
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/ Organism="Arabidopsis thaliana"
/ organism="Arabidopsis thaliana"
/ organism="Barabidopsis thaliana"
/ ecctype="Col-0"
/ db_xref="taxon:3702"
/ clone="Statk" 136266.46.25.x"
/ clone="FCR was performed on Arabidopsis thaliana lines for was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultent fragment for each line was each of determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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BN25.048G14F020110 BN25 Brassica napus cDNA clone BN25048G14, mRNA
sequence.
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Brassica napus
Brassica napus
Spermatophyta; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATGCCACCCATCATATCTACAACAAGCAGAATACACTCTCTCCCATTTGCCGGTAAGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 CCATGCCACCCATCATATTACAACAAGCAGAATACACTCTCTCCATTTGCCGGTAAGTG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AAAAGACTTTGTCAGCAGCTGCTTGTACTCCAAATCACATTTTGCATTCCTTATCCATAA 240
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                             Arabidopsis Genome
Unpublished (2001)
Unpublished (2001)
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckerogealk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g02580.
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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Best Local Similarity
Matches 279; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamida; Solanales; Solanaceae; Solanum.

E (bases 1 to 869)
S Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTS from abiotic stressed potato tissue
Unpublished (2003)
Other_ESTS: EST710577
Conteat: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-arraydeigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: GTA ATA GGA CTC ACT ATA GGG C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2262 TCTCTATAAGCATCTCCATGCTACCCATCATGTACAACAAGCAAAACACACTCTCC 2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 GCCTTGGTATACACTTTTCCCAACTGTCTCTGAGTATATGATCGAGCGTGGTTGGACCAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 ATGTTACTCTACACTTGACCAATTCAACTGGTTCCTCTGTTTTGTTTACATCGTGCTCTA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 TCTTTTATAGTTGAGTTTGGTATGTATTTGGTTCACAAAGGGCTTCATGACATGACATTAAATT 475
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Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 AGATTCTATTCCTACAAGAAAGGCAATGATTCAGCAAATACATGGCAGTGAAGGGTAT
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Pred. No. 4.8e-46;
0; Mismatches 37
                                                                                                               1. .644 // Capanism="Brassica napus" // mol type="mRNA" // cultivar="Jet Neuf" // db_xref="taxon:3708" // clone="RN5041B07" // tissue type="seed" // clone_lib="BN45"
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Solanum tuberosum
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Best Local Similarity 88.0%;
Matches 272; Conservative
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Best Local Similarity
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/tissue type="abiotic stress treated leaf and root tissue"
/lab host="Unblob-TonA"
/clone lib="potato abiotic stress cDNA library"
/clone lib="potato abiotic stress cDNA library"
/note="Vector: pdw/Sport6.1; Site 1: BCoR1; Site 2: Not1;
supplier: Solanum tuberosum var. Rennebec plants were
grown from cuttings on a l6hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed plants were harvested after
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2142 ATGITACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTA 2201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACATAGCACTCATATTCCTGGAAGCCTTATGGACAGCTAATATTCATGACTGCATACAT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GCATTCCACCCATTGGATGGA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  789 AGATGCCATACCATCAAAGGAAGCAATGCTTGCAAAATATCAGTTGCTATGAAAGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2082 GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           729 GCCGTGGTACTGTGCCCTTCCATCACTTTCTGAATACATGAAAACGGAATGGACCAA
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/organism="Solanum tuberosum"

/mol\_type="mRNA"

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Matches 424; Conservative
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/tiseue_Texon:413"
/clone="POACQ30"
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/lab host="DH108-Tona"
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/clone_lib="potato abiotic stress cDNA library"
/clone_lib="potato abiotic stress cDNA library"
/clone_lib="potato abiotic stress cDNA library"
/clone_lib="potato abiotic stress conditions were applied to grown from cuttings on a 16hr light/8 hr dark cycle at 25 c for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set linvolved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the sall stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were grown under the standard conditions and then were cold stressed plants were harvested after cessetion of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-teressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solanum tuberosum (potato)
Solanum tuberosum (potato)
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Solanales; Solanales; Solanace; Solanum.
El (Abases It ob 220)
Suell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from abiotic stressed potato tissue
Lu Unpublished (2003)
Other ESTs: EST716069
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tig.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seg primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
                                                      2681
                                                                                                                                                                                                                                                                                                                                    CK269990 920 bp mRNA linear EST 03-AUG-2004 EST716068 potato abiotic stress CDNA library Solanum tuberosum CDNA CLORE POACQ30 5' end, mRNA sequence.
                                                                                                       216
GGTAAGGTGTGGCCTGTAATGGGTGCCGGCTATCATACCATTCACCATACAACATACCGC 276
                                                 12 hr, 1 d, and 4d. RNA was isolated from equal RNA from each tissue and stress was construct the CDNA library. RNA sample."
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/mol_type="mRNA"
/cultivar="Kennebec"
                                                                                                                                                           2682 TTAGCAGAAAAGACA 2697
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KEYWORDS
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7.8%; Score 228.4; DB 7; Length 920; 62.7%; Pred. No. 4e-41;

Query Match Best Local Similarity

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BETTIES 103-AUG-2004
ESTIGST DOTATO Abjotic Stress CDNA library Solanum tuberosum CDNA CLONE POABTOG 5' end, mRNA sequence.
                                                                                           2081
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1 (Dases 1 to 924)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue Unpublished (2003)
Other_ESTs: EST710578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 ATGITITGCGAGAATAAGTGATGTTGGATGGCCTACCTACATCAATGCGGCTATTTA 483
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                                                                                                2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTAŢ
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Mismatches 166; Indels
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The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
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Solanum tuberosum
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CK264499
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753 bp mRNA linear EST 14-MAY-2005
24RDBNH UP 023 G12 12JAN2004 084 Brassica napus 24RDBNH Brassica
napus cDNA 5′, mRNA sequence.
                                    2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTTA 2201
                                                                                                                                                                                           792 GGTAAGGTGTGGCCTGTAATGGGTGCCGGCTATCATACCATTCACCATACAACATACCGC 851
                                                                                                                                                                                                                                                                            /clone lib="Brassica napus 24RDBNH"
/note="Vector: pDNR-LIB CREATOR; Site_1: Sfi I A; Site_2:
Sfi I B; Zygotic embryos at heart stage from Brassica
napus seeds were used for the isolation of PolyA RNA and
in the construction of the CDNA library. Sequences have
been trimmed to remove vector and low quality regions
using LUCY sequence cleanup software (www.tigr.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Argithciccacaderacccaacrcacciccarccicractrratrcaarcccacara 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                CATAACTATGGTCATTATACCATATGGATGGACTGGATGTTTGGCTCTTTATGGTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 753)
Xiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R.
Gene Expression Patterns during Brassica Zygotic Embryogenesis
Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Raju Datla
Molecular and Devalopmental Genetics
Molecular and Devalopmental Genada
National Reearch Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Raju.Datla@nrc-cnrc.gc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 753.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:3708"
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Brassica napus
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                                                                                                                                                                                                                                                           /tissue type="abiotic stress treated leaf and root tissue"
/lab_host="ubilion="abiotic stress cDNA library"
/clone lib="potato abiotic stress cDNA library"
/note="Vector: pGWNSport6.1; Site_I: BCORI; Site_2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3.4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set I involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 3d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATACGTGGCAATGAAGGCTAT 2081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2142 ATGITACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTTA 2201
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Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/ .
Seg primer: ATT TAG GTG ACA CTA TAG.
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Pred. No. 8.3e-41;
0; Mismatches 165; Indels 86; Gaps
                                                                                                                                /organism="Solanum tuberosum"
/mol_type="mRNA"
/culfivat="Kannebec"
/db xref="taxon:4113"
/clone="POABT06"
                                                                                 Location/Qualifiers
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ATACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCTATAACA 2501	2442	ò
GGGCTTGCGTTTCACCCACTAGACGGG 638	612	qq
TGACTICITIACTIGAIGITITICGGGTTTTCAGGGCTCGCATICCATCCGCTGGACGGG 2441	2382	È
CITTGCC	605	qq
ATTTGCCGGTATGTCAAAGCTATATGTTCTCAATTCTAAGTTCAAGAGCTTGTATCAATGG 2381	2322	È
TCTCTATAAGTATCTCCATGCCACCCATCATATCTACAACAAACA	545	qq
TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAACACACAC	2262	ò
TCTTGTTTTAGTCGAGTTTGGTATTTATTGGATGCACAGAGAGCTTCATGACATTAAGCC 544	485	qq
TCTIGITTIAGTIGAGTITATGATTIAGGSTICACAAAGAGCTICATGACATTAAATI 2261	2202	ò

Search completed: March 7, 2006, 12:18:47 Job time: 11155 secs

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March 7, 2006, 09:11:04; Search time 504 Seconds (without alignments) 10316.206 Million cell updates/sec
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| Cgn2 6/ptodata/1/ina/1_COMB.seq:*
| Cgn2 6/ptodata/1/ina/5_COMB.seq:*
| Cgn2 6/ptodata/1/ina/6_COMB.seq:*
| Cgn2 6/ptodata/1/ina/RB_COMB.seq:*
| Cgn2 6/ptodata/1/ina/HB_COMB.seq:*
| Cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
| Cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
| Cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
| Cgn2 6/ptodata/1/ina/PP_COMB.seq:*
| Cgn2 6/ptodata/1/ina/PP_COMB.seq:*
| Cgn2 6/ptodata/1/ina/RB_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          1303057 seqs, 888780828 residues
GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7458, Ap 14, Appl 11, Appl 1357, Appl 1318, Ap 22, Appl 2275, Appl 901, Appl 53, Appl 29, Appl 23, Appl 25, Appl 9, Appli 4514, Ap 379, App Sequence 23, 53, 13, Description Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence US-09-443-0411A-27 US-09-443-0411A-29 US-09-443-0411A-29 US-09-443-0411A-9 US-09-313-294A-4514 US-09-313-294A-7458 US-09-313-294A-7458 US-09-443-0411A-13 US-09-443-0411A-13 US-09-443-041A-11 US-09-443-041A-15 US-09-443-041A-15 US-09-902-540-1357 US-09-902-540-1357 US-09-902-540-1280 US-09-903-540-1280 US-09-949-016-901 US-09-949-016-901 US-09-949-016-901 US-09-949-113-50-53 US-09-868-53 US-09-98-53 US-09-98-53 SUMMARIES Query Match Length DB 11175 11447 11447 1110 10070 26070 26070 26070 2617 4959 4959 4959 11141 11039 2005 2005 396 396 396 Result U

AGCTTCAAGAAAGCAGAGTGAGGATGCCCACTTGGGGGTTGTTCTTCTGTGTTGTTTTTT 1002

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GTTGTTGTTCAAAGTTTCAGCCTTTCTTGTTCTTTTTTCTTCTTCTTCTTATTCATGT

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GGATACCATACGATACACCACACACATACAAGCATAACTATGGTCATTATACCATATGG

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GGATACCATACGATACACCACACGACATACAAGCATAACTATGGTCATTATACCATATGG ATGGATTGGATGTTTGGCTCTCTTAGGATCCTCTCTTAGAAGAAGATGACAAAAGAC 819

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GCGCTGTTTATAGGGCCAATTCATTTCACAACTCATATAGGTCTTTTGTTCATGGAAGCG

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GCGCTG-TTATAGTGCCAATTCATTTCACAACTCATATAGGTCTTTTGTTCATGGAAGCG

ATATGGACGGCGAACATCCATGACTCCATCCCATGCCAACATCTGGCCAGTAATGGGTGCA ATATGGCGGCGGAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA

	Sequence 113, App Sequence 1, Appli Sequence 595, App Sequence 17091, A Sequence 2813, Ap Sequence 2, Appli Sequence 17394, A Sequence 17395, A Sequence 17395, A Sequence 12, Appl Sequence 25, Appl Sequence 25, Appl Sequence 12091, A Sequence 12091, A Sequence 12091, A	MENTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS 723	15.8%; Score 461; DB 3; Length 1175; imilarity 97.6%; Pred. No. 3e-108; ; Conservative 0; Mismatches 10; Indels 2; Gaps 2; TTTACAGGGCTTGCA-TTCACCCAGTAGACGGATACTTAAGGCTGTACCGCATGTGATA 520
US-08-628-417-6 US-09-806-708B-22 US-09-973-278-700 US-09-949-016-14017 US-09-949-016-12643	US-09-614-221A-113 US-09-815-811-1 US-08-938-416-595 US-09-949-016-17091 US-09-621-976-18648 US-09-621-976-18648 US-09-949-016-17394 US-09-949-016-17394 US-09-949-016-14273 US-09-668-097A-13 US-09-668-097A-13 US-09-668-097A-13 US-09-668-097A-13 US-09-68-097A-13 US-09-68-097A-13 US-09-68-097A-13 US-09-68-097A-13 US-09-248-016-14273 US-09-68-097A-13 US-09-68-097A-13	11S 11S 85,	15.8%; Score 461; DB 3; Length 1175; imilarity 97.6%; Pred. No. 3e-108; ; Conservative 0; Mismatches 10; Indels 2; Gaps TTTACAGGGCTTGCA-TTCACCCAGTAGACGGGATACTTAAGGCTGTACCGCATGTGATA
0 m m m m n		. US/0988 ppany NSGENIC .1 .1 .1 .001-06-2 .3 .1on 3.0	88; 68; -TT
N	.8 1098 .7 1689 .7 41736 .7 41736 .7 282 .7 282 .7 5852 .6 145241 .6 145241 .6 5000 .6 1662 .6 5000 .6 5000	-23 6822142 CORATION: CORATION: MONBANTON: INVENTION: TRANSGENIC PENCE: ENCE: MTCG73.1 ENCE: MTCG73.1 CING DATE: 2001-06-20 SEQ ID NOS: 33 PatentIn version 3.0 3.175 Arabidopsis thaliana -23	15.8%; Conservative ACAGGGCTTGCA-TT
नं नं नं नं नं नं		ppli 2142 2142 2142 2142 NTIC CATM ID ID abid	Similarity 19; Conser: TTTACAGGG
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0.000 4 4 4 4 4 4 4 6 0.000 8 8 8 8 4 4 4 4 4 4 4 6 6 6 8 8 6 6 6 6	RESULT 1  S09-885-723-23  Squence 23, Application US/09885723  Patent No. 6822142  GENERAL INFORMATION:  TITLE OF INVENTION: TRANSGENIC PLAN:  FILE REFERENCE: WTC6783.1  CURRENT PILING DATE: 2001-06-20  NUMBER OF SEQ ID NOS: 33  SOFTWARE: Patentin version 3.0  SOFTWARE: Patentin version 3.0  SEQ ID NO 23  LENGTH: 1175  TYPE: DAA  ORGANISM: Arabidopsis thaliana US-09-885-723-23	atch cal S 489 462 643
32222		RESULT US-09-8 US-09-8 Seque Paten GENER APPL TITL FILE CURR CURR CURR NUMB SEQ I LEN CORP CORP CORP CORP CORP CORP CORP CORP	Query M Best Lo Matches
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                                         2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTAA 2201
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710 CATTIGGCCCTCATATICATIGAGGGCGTTIGGACTGCAAATATICATGATIGCATICAT 769
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Pred. No. 4.2e-38;
0; Mismatches 175; Indels
                                                                                                                                                                                                                                                         Sequence 29, Application US/09443041A
Fatent No. 6465717
GENERAL INFORMATION:
APPLICANT: Famedu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
FRIOR APPLICATION NUMBER: 60/109,283
FRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
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; OTHER INFORMATION: any nucleotide
US-09-443-041A-29
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Best Local Similarity 59.81
Matches 389; Conservative
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US-09-443-041A-29
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                                                                GTCTCTCTCAACCTTTCCAATTATATTGTTACAAACATTTGCTGTCTAGTTTAAAACATG
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                                                                                                                                                                                                                                              RESULT 2
US-09-443-041A-27
US-09-443-041A-27
Sequence 27, Application US/09443041A
Fatent No. 6465717
GENERAL INFORMATION:
APPLICANT: Remodu, Omolayo O.
APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Refalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR PRILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 27
SEQ ID NO 27
LENGTH: 1447
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                                                                                                           471 GIGITATGITAATATCAGTGAAGTTGGCCAATGTACCTGGTTTATCTGGCTTTATA
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                             468 ACATCGCTCTCGTGTTCTTGGAGGCGTGTGGACGACAAACATCCACGACTGCATTCACG
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58.6%; Pred. No. 6.3e-36;
iive 0; Mismatches 189;
                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/09443041A
Patent No. 6465717
GENERAL INFORMATION:
APPLICANT: Pamodu, Omolayo O.
APPLICANT: Pamodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE NOF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE: 1999-11-18
CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1999-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 25
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Best Local Similarity 58.6
Matches 389; Conservative
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; ORGANISM: Oryza sativa
US-09-443-041A-25
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                                                                                                      IGTTACTCTACACTTGACCATTTCAACTGGTTCCTCTGTTTCCTCTACATAGCTCTCTAT 2202
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                    407
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                                                                                                                                            642 GGCAAGATCTGGCCGCTGATGGGCGCCGCTACCACCATCCACCACACGACGTACCGG 701
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Best Local Similarity 59.8%; Pred. No. 6.7e-38;
Matches 388; Conservative 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09443041A
Patent No. 6465717
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR PPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
LENGTH: 911
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RESULT 7
US-09-313-294A-4514

is Sequence 4514, Application US/09313294A

j Sequence 4516212

j GENERAL INFORMATION:
    APPLICANT: Lalgudi, Raghunath V.
    APPLICANT: Lalgudi, Raghunath V.
    APPLICANT: Sherman, Bradley K.
    TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
    FILE REFERENCE: PL-0017 US
    CURRENT APPLICATION NUMBER: US/09/313,294A
    CURRENT FILING DATE: 1999-05-14
    NUMBER OF SEQ ID NOS: 7600
    SOFTWARE: PERL PROGRAM
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                                                                                                                  2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAAGCAAAACACACTCTCTCC 2321
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575 TCTCATTTTTGTGGAGTTTGGAATTTACTGGATGCACAGAGAGTTGCATGACATAAAGCC 634
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; OTHER INFORMATION: Incyte ID No. 6476212 700348549H1
US-09-313-294A-4514
                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 GTTTG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Pamodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
ITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/443,041A
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
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NAME/KEY: unsure
LOCATION: (885)
OTHER INFORMATION: any nucleotide
NAME/KEY: unsure
LOCATION: (949)
OTHER INFORMATION: any nucleotide
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OTHER INFORMATION: any nucleotide
NAME/KEY: unsure
LOCATION: (1050)..(1051)
OTHER INFORMATION: any nucleotide
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SOFTWARE: Microsoft Office 97
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SEQ ID NO 9
LENGTH: 1070
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US-09-443-041A-9
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Sequence 7458, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPRENCE: PL-0017 US
CURRENT APPLICANT: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 7458
LENGTH: 314
                                                                                                                                                                                      1524 GATTATAATGATCAGATCGTCAATGAGACCTCTTTTTACAACCGAATGGTTCTGAGTCAC 1583
                                                                                                                                                                                                                                                                                               1584 CTTTTGCCGGTGAATCTATGGGAACCTTTACCACATTTCCTCCAGACATGGCTCCGGAAC 1643
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2.8%; Score 82.8; DB 3; Length 3:
Best Local Similarity 60.8%; Pred. No. 2.4e-11;
Matches 135; Conservative 0; Mismatches 87; Indels
                                                                          Score 90; DB 3; Length 459
Pred. No. 4.1e-13;
0; Mismatches 70; Indels
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; OTHER INFORMATION: Incyte ID No. 6476212 700381763H1
US-09-313-294A-7458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1704 TA-CCTTAAACTCAACGTTTACGTCCCCAAAGGT 1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 TATTGGGAAGCGCAACGTTCATGTCCCCAAAGAT 313
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                                                                               3.1%;
                                                                                                                                Matches 143; Conservative
ORGANISM: Glycine max
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-313-294A-7458
        ; ORGANISM: GLY.
US-09-443-041A-13
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                                                                                                                                                                                         Sequence 379, Application US/09313294A
Sequence 379, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICAMT: Lalgudi, Raghunath V.
APPLICAMT: Ito, Laura
APPLICAMT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENTE: PL-017 US/09/313,294A
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
SEQ ID NO 379
LENGTH: 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700549111H1
NAME/KEY: ungure
LOCATION: 5
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| Sequence 13. Application US/09443041A
| Patent No. 6465717
| GENERAL INFORMATION:
| APPLICANT: Famodu, Omolayo O. APPLICANT: Rafelski, Antoni
| APPLICANT: Shen, Jennie | TITLE OF INVENTION: Sterol Metabolism Enzymes | TITLE OF INVENTION: Sterol Metabolism Enzymes | TITLE OF INVENTION: Sterol Metabolism Enzymes | TITLE OF INVENTION: Sterol Metabolism Enzymes | TITLE OF INVENTION: Sterol Metabolism Enzymes | TITLE OF INVENTION: Sterol Metabolism Enzymes | TITLE OF INVENTION: Sterol Metabolism Enzymes | TURRENT FILING DATE: 1999-11-18 | PRIOR FILING DATE: 1998-11-20 | NUMBER OF SEQ ID NOS: 33 | SEQ ID NOS: 33 | LENGTH: 459 | TYPE: DNA
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                         2648 GATGGACTGGATGTTTGGCTCTCT 2671
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                                                              248 GATGGACTGGATGTTTGGTACGCT 271
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ORGANISM: Zea mays
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1602 TOGGAACCTITACCACATITCCTCCAGACATGGCTCCGGAACTACCTCGCCGGAAACATA 1661
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                                                                                                                                                                                                                                                                                                             APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
                                                                                                                                                                            Sequence 15, Application US/09443041A Patent No. 6465117 GENERAL INFORMATION:
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OTHER INFORMATION: any nucleotide
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OTHER INFORMATION: any nucleotide
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INFORMATION: any nucleotide
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; OTHER INFORMATION: any nucleotide
US-09-443-041A-15
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SEQ ID NO 15
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Best Local Similarity
Matches 95; Conserv
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APPLICANT: DORNER, F. APPLICANT: SCHEFLINGER, F. G.
APPLICANT: SCHEFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESSER: FOLEY & Lardner
ADDRESSER: Foley & Lardner
STREET: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 77.8; DB 2;
ilarity 6.1%; Pred. No. 1.9e-09;
Conservative 236; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REGISTATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base palrs
                                                                                                                                                                                                                                                                                                                                           ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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(703)683-4109
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STRANDEDNESS: single
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Matches 25, Conserv
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Patent No. 683347
GENERAL INFORMATION:
APPLICANT: GOldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Missend, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT PELICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
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RESULT 13
US-09-443-041A-11
US-09-443-041A-11
US-09-443-041A-11
Sequence 11, Application US/09443041A
SECTION 6465717
GENERAL INFORMATION:
APPLICANT: Femedu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:

; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

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CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
SEQ ID NO 11
TYPE: DNA
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SEQ ID NO 1357
LENGTH: 612
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US-09-443-041A-11
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LOCATION: (1)..(6
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DB 3; Length 612;

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Query Match

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Fatent No. 683347

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Miggand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPRENCE: 38-10 (15849)B
CURRENT TILING DATE: 2001-07-10
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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                                               0; Mismatches 137; Indels
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Pred. No. 1.7e-05;
52.1%; Pred. No. 2.1e-07;
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; OTHER INFORMATION: unsure at all n locations US-09-902-540-1318
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                                               Matches 149; Conservative
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Matches 150; Conservative
Best Local Similarity
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US-09-902-540-1318/c
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Search completed: March 7, 2006, 13:20:15 Job time : 509 secs

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/ cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-736-318-22
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Sequence 13, Appl Sequence 220, App Sequence 36195, A Sequence 36196, A Sequence 36196, A Sequence 15, Appl Sequence 11, Appl Sequence 5880, A Sequence 5880, A Sequence 5279, A Sequence 5589, A	Sequence 2372, Ap Sequence 185, App Sequence 1995, Ap Sequence 2, Applis Sequence 2, Applis Sequence 1176, A Sequence 81106, A Sequence 81106, A
US-10-224-880C-13 US-09-294-093B-220 US-10-363-345A-36195 US-10-363-45A-36195 US-10-363-483A-36196 US-10-363-483A-36196 US-10-24-880C-15 US-10-214-880C-11 US-10-24-880C-11 US-10-24-880C-11 US-10-425-115-58802 US-09-923-876-5279 US-09-923-876-5279 US-09-923-876-5279 US-09-923-876-5279 US-09-923-876-5279	US-10-311-455-2372 US-09-960-352-573 US-10-239-676-185 US-10-311-455-1995 US-10-312-841-2 US-10-437-963-72176 US-10-425-115-81106 US-10-311-455-894
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## ALIGNMENTS

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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                           APPLICANT: Choe, Sunghwa
APPLICANT: Choe, Sunghwa
TITLE OF INVENTION: Dwf7 MUTANTS
FILE REPERRNCE: 2225-0003
CURRENT APPLICATION NUMBER: US/09/775,879
CURRENT APPLICATION NUMBER: 60/179,901
PRIOR APPLICATION NUMBER: 60/179,901
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ 1D NOS: 25
SEQ 1D NO 22
Sequence 22, Application US/09775879
Patent No. US20020068822A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 2925; Conservative
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CORGANISM: Genomic HDF7
US-09-775-879-22
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AGAAAGGCTAGAATTATATAAATGTCAGCTGCA 	AGACTICIGACTIAACCAGAGTITAGAICTITGIGITICTCTCTCTGGTCTCGGACTGAIT 3	ggaaatgacgagagttctttattattacttcctggagtgtatcttggttaatccaagga 4 	rctaaatattacttgtaacttccttacgtttttgtttacagggcttgcattca 	481 CCCAGTAGACGGGATACTTAAGGCTGTACCGCATGTGATAGCGCTGTTATAGTGCCCAATT 540	541 CATTICACAACTCATATAGGTCTTTTGTTCATGGAAGCGATATGGACGGCGAACATCCAT 600 	601 GACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCAGGATACCATACGATACCACCAC 660	661 ACGACATACAAAGCATAACTATGGTCATTATACCATATGGATGG	721 CTTAGGGATCCTCTTAGAAGAAGATGACAACAAAGACAGCTTCAAGAAAGCAGAGTGA 780 	781 GAATGCCCACTTGGGGTTTTGTTCTTCTGTTTTGTTGTTGTTGTTCTTGTTCTAAAGTTTC 840	841 AGCCTTTCTTGTTCTTCTTCTTCTTATTCATGTGTCTCTCTAACCTTTCCAAT 900	901 TATAITGTTACAAACAITTGCTGTCTAGTTTAAAACATGTAAATGTTTGATGATCTTTGC 960 	961 AAGACTCCATTTTGTTTAAGGTAAACCTTGAATCTCATAGATTGTCGATTGTTGGTATT 1020 	1021 TCCATTTTCAGGTACGGTTCTGTAGACTGTAGTCTTGCTGACCAGTCCGGCTTAACCACC 1080	1081 CCAAATTTCAAAGATCTCACCAATCAAAATGCTGGCTGGC	1141 GITAATCCGTCTAGCTTTACTCTTTAGACCTACCTTAGACAGTTAGACACCTGCTAATTA 1200 	1201 AIGAGITICCTITITICITGITCAGCAAGTIACCIGIGITACITGAGGITGAGITAANGG 1260 1201 AIGAGITICCTITITCITGITCAGCAAGITACCIGIGITACITGAGAGFIGAGITAANGG 1260	1261 TAGTAAACGCAATTTAACCCTTATAAGTTTAATCGTATTCAACGAATGACCCAGAGACTT 1320 1261 TAGTAAACGCAATTTAACCCTTATAAGTTTAATCGTATTCAACGAATGACCCAGAGACTT 1320 1321 TAAATAAATCATCGTAACCCTCCACTTCAAATTCTTTTAAAAAGTAGCAAATCATTT 1380	
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                                                                                                                Gaps
                                                                                                               3,
                                                                                     Length 1889;
                                                                                                               Indels
                                                                                  Score 924.4; DB 7;
Pred. No. 5.6e-204;
                                                                                                               0; Mismatches
                            TYPE: DNA ORGANISM: Genomic dwf7 (Arabidopsis)
                                                                                   31.6%;
99.6%;
                                                                                                               Matches 958; Conservative
                                                                                     Query Match
Best Local Similarity
    SEQ ID NO 20
LENGTH: 1889
                                               ; ORGANISM: GEI
US-10-736-318-20
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| Publication No. US20040133948A1
| GENERAL INFORMATION: ABPLICANT: Choe, Sunghwa APPLICANT: Choe, Sunghwa APPLICANT: Choe, Sunghwa TITLE OF INVENTION: DWFT MUTANTS
| TILE REPERBNCE: 2225-0003
| CURRENT FILING DATE: 2003-12-15
| PRIOR PILING DATE: 2001-02-02
| PRIOR PILING DATE: 2001-02-02
| PRIOR PILING DATE: 2000-02-02
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Best Local Similarity 97.6%; Pred. No. 2.3e-96;
Matches 489; Conservative 0; Mismatches 10;
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Patent No. US20020160378A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION UNMBER: US/09/938,842A

CURRENT FILING DATE: 2000-08-24

PRIOR PELLING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22
CURRENT APPLICATION NUMBER: US/10/862,907
CURRENT FILING DATE: 2004-06-07
PRIOR APPLICATION NUMBER: US/09/885,723
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 23
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; ORGANISM: Arabidopsis thaliana
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Sequence 23, Application US/09885723

Sequence 23, Application US/09885723

Sequence 23, Application US/09885723

Sequence 23, Application US/09881

Sequence 23, Application US/09881

Sequence 23, Application US/09/881

TITLE OF INVENTION: TRANSCENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS TITLE OF INVENTION NUMBER: US/09/885,723

CURRENT FILING DATE: 2001-06-20

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.0

SEQ ID NO 23

LENGTH: 1175
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Publication No. US20050086713A1
GENERAL INFORMATION:
APPLICANT: MONBENIC COMPANY
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS
FILE REFERENCE: MTC6783.1
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Pred. No. 5.7e-70;
0; Mismatches 108;
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 421
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                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Arabidopsis thaliana
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72.4%;
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Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILLE OF INVENTION: SAME, AND METHODS OF USE
FILLE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
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Pred. No. 5.7e-70;
0; Mismatches 108;
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US-09-938-842A-421
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Best Local Similarity 72.4%;
Matches 508; Conservative
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  NUMBER OF SEQ ID
SEQ ID NO 421
LENGTH: 846
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Query Match 6.9%;
Best Local Similarity 61.1%;
Matches 397; Conservative (
                                                                                                                                            TYPE: DNA
ORGANISM: Sorghum bicolor
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                                                                                                                                                                                                                                                                    Query Match 7.0%; Score 203.4; DB 6; Best Local Similarity 61.3%; Pred. No. 2e-36; Matches 399; Conservative 0; Mismatches 166;
APPLICANT: Orozco, Emil M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Shen, Jennie B.
TITLE CO INVENTION: Sterol Metabolism Enzymes
FILE REPERENCE: BB1282 US DIV
CURRENT APPLICATION NUMBER: US/10/224,880C
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 27
LENGTH: 1447
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                                                                                                                                                                                                          type: DNA Clycine max OS-10-224-880C-27
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APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua

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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REPERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 13122
LENGTH: 1002
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US-10-767-701-13122
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Pred. No. 7.6e-36;
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Publication No. US20040010815A1
GRNERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Lange, Markus B.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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2082 GCCTTGGTACACTCTTCCTTCCAGCTGTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 188; DB 6; Length 1135;
Pred. No. 6.8e-33;
0; Mismatches 175; Indels 8
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CURRENT FILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2002-04-04

PRIOR PLING DATE: 2002-04-04

NUMBER OF SEQ ID NOS: 662

SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
                                                                                                                                      Sequence 530, Application US/10259194A Publication No. US20040010815A1 GENERAL INFORMATION:
                                                                                                                                                                                               : Lange, Markus B.
Ghassemian, Majid
Bhiggs, Steven P.
Cooper, Bret
Glazebrook, Jane
Goff, Stephen A.
Karagiri, Pumiyaki
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Provart, Nicholas
Ricke, Darrell
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; ORGANISM: Triticum aestivum
US-10-259-194A-530
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Best Local Similarity
TAG 2685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                           PLANT GENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 833;
                                             APPLICANT: ALGE, OUGLA
APPLICANT: Mondamer, Todd
APPLICANT: Mondamer, Todd
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: COURTENT APPLICANT: COURTENT APPLICANTION NUMBER: US/10/259,194A
CURRENT APPLICANTION NUMBER: US 60/325,277
FRIOR PRICHAS APPLICATION NUMBER: US 60/375,277
FRIOR FILING DATE: 2002-04-04
FRIOR FILING DATE: 2002-04-04
FRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SEQ ID NO 287
SEQ ID NO 287
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                                                                                                                                         IDENTIFICATION AND CHARACTERIZATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 189.4; DB (
Pred. No. 2.7e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.5%;
Best Local Similarity 59.3%;
Matches 393; Conservative
                   Fumiyaki
Stephen A
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Oryza sativa
                                    Kreps, Joel
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2383 GACTICITIACITGAIGITITICGGGITITICAGGGCICGCATICCATCCGCIGGACGGGA 2442
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                                                                                                                                                                                                                            2502 CATCTGAGTCTTTTTGGAAGGGATATGGACAGCAAGCATCCATGATTGCATACAT
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US-10-224-880C-23
Sequence 23, Application US/10224880C
Sequence 23, Application US/10224880C
Publication No. US20030229914A1
GENERAL INFORMATION:
APPLICANT: Famedu, Omolayo O.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Shen, Jennie B.
TITLE NOFINVENTION: Sterol Metabolism Enzymes
FILE REFERENCE: BB1282 US DIV
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR PILING DATE: 1999-11-20
NUMBER: OF SEG ID NOS: 33
SOFTWARE: Microsoft Office 97
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59.8%;
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Best Local Similarity 59.8
Matches 388; Conservative
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; ORGANISM: Zea mays
US-10-224-880C-23
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                                                                                                                                       CATCIGAGICITITIGGAAGGGATATGGACAGCAACCATCCATGATTGCATACAT 2561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTCATCTTTGTGGAGTTCGGAATTTACTGGATGCACAGAGAGTTGCATGACATAAAGCC 427
                                                              554 ATACTGCAAGCCATATCGCACGTGATTGCTCTTCTTCTCCCGATGCACTTCAGGACG 613
                                                                                                                                                                                                  614 CACATTGCTCCTATTCATAGAGGCGGTGTGGACGCCAAACATCCACGACTGCATCCAC 673
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                                                                                                                                                                                                                                                                    2082 GCCTIGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                               CACAACTATGGCCACTACACCGTGTGGGATGGACTGGTTTGGCACCCT 783
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0; Mismatches 175;
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| Publication No. US20030229314A1
| GENERAL INFORMATION:
| APPLICANT: Famodu, Omolayo O. |
| APPLICANT: Pamodu, Denil M. |
| APPLICANT: Rafalski, J. Antoni APPLICANT: Shen, Jennie B. |
| TITLE OF INVENTION: Sterol Metabolism Enzymes FILE REFERENCE: BB1282 US DIV |
| TOTRENT APPLICATION NUMBER: US/10/224,880C |
| CURRENT FILING DATE: 1998-11-20 |
| PRIOR APPLICATION NUMBER: 60/109,283 |
| SOFTWARE: Microsoft Office 97 |
| SEQ ID NO S: 33 |
| SEG ID NO S: 39 |
| SEG ID NO S: 39 |
| SEG ID NO S: 39 |
| SEG ID NO S!
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US-10-224-880C-29
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2322 ATTIGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGG 2381
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                       2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAAGAAAAAACACACTCTCC 2321
                                                                                                                                                                                                                                                                                                                                                                                                                          688 GCCAAGATATGGCCAGTCATGGCTGCTGGATATCACCATTCACCATACGACATACCGC 747
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                                                                   474 ATTATACAAATATCTGCATGCAACCCACCATATTTACAACAAGGAGAATACCTTGTCTCC
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-----TGGACTCGCGTTTCACCCACTGGATGGTA 407
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                                                                                                                                   408 TTCTGCAAGCGATACCGCATGTGCTTTGCGCTCTTCCTCCCAACGCACTTCAGGACGC
                                             2443 TACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCGATTCATCTCATAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 AGATGCCATCCCCACAAATGAAGCTATGAAGAAGCAAATAGTTGTAGCATCGAAGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 184.4; DB 6; Length 828;
Pred. No. 4e-32;
0; Mismatches 186; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                     2623 ATAACTATGGTCATTATACCATATGGATGGTGGATGTTTGGCTCTCT 2671
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FRIOR APPLICATION NUMBER: US 60/325,277

FRIOR FILING DATE: 2001-09-26

FRIOR APPLICATION NUMBER: US 60/370,743

FRIOR APPLICATION NUMBER: US 60/370,620

FRIOR FILING DATE: 2002-04-04

NUMBER OF SEQ ID NOS: 662

SOFTWARE: PATCHLIST, PATCHLIST, DI VETSION 3.0.4 (C) 2001 Syngenta

SEQ ID NO 608

LENGTH: 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 608, Application US/10259194A
Publication No. US20040010815A1
GENERAL INPORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Bret
APPLICANT: Gozer, Caper,
APPLICANT: Gate, Stephen A.
APPLICANT: Katagiri, Fumiyaki
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Best Local Similarity 59.0%;
Matches 392; Conservative (
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ORGANISM: Zea
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March 7, 2006, 09:28:50 ; Search time 809 Seconds (without alignments) 7927.094 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result		Query				
Š.	Score	Match	Match Length DB	8 :	DI	Description
-	54.2	1.9	3641	12	US-11-102-026A-181	Sequence 181, App
U	53.8	1.8	305312	8	US-10-995-561-13236	Sequence 13236, A
7	52.8	1.8	8537	æ	US-10-240-708-42	Sequence 42, Appl
**	1 22	1.8	5562	œ	US-10-240-708-63	Sequence 63, Appl
<i></i>	51.6	1.8	6326	80	US-10-240-708-57	٠,
w	5.4 51.6	1.8	8607	æ	US-10-240-708-72	Sequence 72, Appl
(-	7 51	1.7	628	9	US-09-925-065A-768903	Sequence 768903,
υ	3 50.8	1.7	664	9	US-09-925-065A-402424	Sequence 402424,
Ü	50.8	1.7	664	9	US-09-925-065A-402425	Sequence 402425,
7	50.2	1.7	5360	æ	US-10-240-708-66	
H	49.8	1.7	613	9	US-09-925-065A-834303	
11	49.4	1.7	613	9	US-09-925-065A-834302	Sequence 834302,
c 13	3 49.4	1.7	2409	œ	US-10-821-234-2	Sequence 2, Appli
1,	49.4	1.7	5152	æ	US-10-240-708-47	Sequence 47, Appl
11	5 49.4	1.7	10166	12	US-11-147-606-3	Sequence 3, Appli
0	5 49	1.7		9	US-09-925-065A-195994	Sequence 195994,
0 17	7 49	1.7	260	9	US-09-925-065A-195995	Seguence 195995,
18	3 49	1.7	6040	œ	US-10-240-708-70	Sequence 70, Appl
15	49	1.7	6801	89	US-10-240-708-62	Sequence 62, Appl
0 20	48.8	1.7	524	9	US-09-925-065A-389544	Sequence 389544,

Seguence 337713,	Sequence 749620,	Sequence 822274,	Sequence 12, Appl	Sequence 34, Appl	Sequence 599143,	Sequence 80, Appl	Sequence 182, App	Sequence 10, Appl	Sequence 133, App	Sequence 278, App	Sequence 33, Appl	Sequence 714408,	Sequence 714409,	Seguence 714410,	Sequence 714411,	Sequence 96, Appl	Seguence 939011,	Sequence 79, Appl	Seguence 2, Appli	Seguence 40, Appl	Sequence 162822,	Seguence 71, Appl	Sequence 808614,	Semience 41. Anni
US-09-925-065A-337713	US-09-925-065A-749620	US-09-925-065A-822274	US-10-240-708-12	US-10-240-708-34	US-09-925-065A-599143	US-10-240-708-80	US-11-091-883-182	US-10-240-708-10	US-10-947-249-133	US-11-000-688-278	US-10-240-708-33	US-09-925-065A-714408	US-09-925-065A-714409	US-09-925-065A-714410	US-09-925-065A-714411	US-11-011-332A-96	US-09-925-065A-939011	US-10-240-708-79	US-10-240-708-2	US-10-240-708-40	US-09-925-065A-162822	US-10-240-708-71	US-09-925-065A-808614	US-10-240-708-41
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1.7	1.7	1.7	1.7	1.7	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6
48.8	48.8	48.8	48.6	48.4	48	47.8	47.6	47.4	47.2	47.2	47.2	47	47	47	47	47	46.8	46.8	46.8	46.8	46.6	46.6	46.4	46.4
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## ALIGNMENTS

US-11-102-026A-181

JS-II-102-026A-181					
; Sequence 181, Application US/11102026A					
; FUDITICACION NO. USZUDBUDZIUS/AI : GENERAL INFORMATION:					
APPLICANT: Monsanto Technology LLC					
, APPLICANT: Baum, James A					
; APPLICANT: Zhang, Bei					
; TITLE OF INVENTION: Compositions and Methods for Control of Insect Infestations in Pl	Control	of Insect	Infest	ations	in Pl
; FILE REFERENCE: 38-21 (53596)					
CURRENT APPLICATION NUMBER: US/11/102,026A					
CURRENT FILING DATE: 2005-04-08					
PRIOR APPLICATION NUMBER: 60560842					
PRIOR FILING DATE: 2004-04-09					
PRIOR FILING DATE: 2004-04-27					
PRIOR APPLICATION NUMBER: 60579062					
PRIOR APPLICATION NUMBER: 60603421					
; PRIOR FILING DATE: 2004-08-20					
PRIOR FILING DATE: 2004-10-11					
; PRIOR APPLICATION NUMBER: 60669241					
; PRIOR FILING DATE: 2005-04-07					
; NUMBER OF SEQ ID NOS: 190					
; SEQ ID NO 181					
; LENGTH: 3641					
TYPE: DNA					
; ORGANISM: Lygus hesperus JS-11-102-026A-181					
1 0% . Score 54 3 . DB 13.		Length 3641.			
Similarity 50.6%: Pred No. 0.5		17500 1			
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US-10-440-100-42

Sequence 42, Application US/10240708

Publication No. US20050282157A1

GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: DY Assessing DNA Methylation
FILE REPRENCE: 5013-1012
CURRENT APPLICATION NUMBER: DC7/EP01/03971
FRIOR PELING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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Publication No. US20050282157A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: DY ASSESSING DISSESSES
TITLE OF INVENTION: DY ASSESSING DAM Methylation
TITLE OF INVENTION: DY ASSESSING DAM Methylation
FILE REFRENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
FRIOR APPLICATION NUMBER: DCT/FR01/03971
FRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 ATTTAAAAAGTTGATTTTGGCGGGGGGGGGGTTTAAGTTTTGGTATTTTAGTAT 309
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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ORGANISM: Artificial Sequence
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Best Local Similarity 48.6%;
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-240-708-42
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OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
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                                                                                        1847 TTTCAGTTCTTGTCTTCTACTTCTCATTTAATTAGTTTTAAAGTTTAATATTTTTGGCTA 1906
                                                                                                                                                                                                                                                                                                                         1907 ATCCACATTTTTAAGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATT 1966
                                                                                                                                                                                                                                                                                                                                                                                IS-10-995-561-13236/c
Sequence 13236, Application US/10995561
Sequence 13236, Application US/2095561
Sequence 13236, Application W. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FactSEQ for Windows Version 4.0
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TCTTGTCTTCTACTTCTATTTAATTAGTTTTAAAGTTTTAATATTTTTGGCTAATCCACA
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49.3%; Pred. No. 3.4;
tive 0; Mismatches 172; Indels 1;
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Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)...(30531;
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LENGTH: 305312
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Matches 138;
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          Query Match
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APPLICANT: PIEFENBROCK, Christian
APPLICANT: PIEFENBROCK, Christian
APPLICANT: PIEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT APPLICATION NUMBER: US/10/3971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PRILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
LENGTH: 6326
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                                                                                                                                                                                                                                                          ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-708-63
                                                                                                                                                                                                                                                                                                                     DB 8; Length 5562
                                                                                                                                                                                                                                                                                                                   Query Match 1.8%; Score 52; DB 8; Length 556
Best Local Similarity 50.7%; Pred. No. 2.4;
Matches 150; Conservative 0; Mismatches 145; Indels
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR PAPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 63
LENGTH: 5562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 57, Application US/10240708 Publication No. US20050282157A1 GENERAL INFORMATION:
                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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US-10-240-708-57
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                                                                                                                                                                                                     TYPE: DNA
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US-10-240-708-72

US-10-240-708-72

US-10-240-708-72

Sequence 72, Application US/10240708

Publication No. US20050282157A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: OLENGERSENCOK, Christian

APPLICANT: OLENGERSENCOK, Christian

APPLICANT: DEPENBROCK, Christian

APPLICANT: DEPENBROCK, Christian

APPLICANT: Disguess of Diseases Associated with DNA Replication

FILE REFERENCE: 5013.1012

CURRENT APPLICANTON NUMBER: US/10/240,708

CURRENT APPLICANTON NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SERVING ON ON NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98
                                                                                                      TICICATITAATITAGITITAAAGITITAATATITITIGGCTAATCCACATITITTAAGITGA 1926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8607;
  Length 6326;
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Pred. No. 3.2;
0; Mismatches 139;
Score 51.6; DB 8;
Pred. No. 3;
                                                      0; Mismatches 144;
  1.8%;
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ORGANISM: Artificial Sequence
                                                      Conservative
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Matches 146; Conservative
                           Similarity
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ATCTTCCATGAAATTTGAGCTCAAAATATACCATGAA-ATTGAAATTTGTGGTTCTTAGT 1985
                                                                            1654 GAAACATACTCTACTTCATCTCCGGCTTCCTCGGTGCTTCTACATCTATTACCTTAAAC 1713
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Unclectede Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-66

PRIOR FILING DATE: 2001-01-66

PRIOR FILING DATE: 2001-01-66

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PRIOR FILING DATE: 2001-01-66

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US-09-925-065A-402424/c

US-09-925-065A-402424, Application US/09925065A

; Sequence 402424, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: NUCLEOCIDE POLYMOTPHISMS in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A
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                                                                                                                                                                TCTATTTCTTGCTTGGTTTCTTCTTTTTTGTGGTTAGAATCCATT 2031
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ilarity 51.7%; Pred. No.
Conservative 1; Mismatcl
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US-09-925-065A-768903
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Best Local Similarity
Matches 140; Conservi
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Pred. No. 2.2;
1; Mismatches 153; Indels
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PABLESEQ for Windows Version 4.0
SEQ ID NO 402424
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 402425
LENGTH: 664
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Best Local Similarity 48.0%;
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; ORGANISM: Homo sapiens
US-09-925-065A-402424
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US-09-925-065A-402425
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1984 GITCTATITCTIGCITGGITICTTCTATITITIGIGGITAGAAICCATICCTACGAGAAG 2043
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       TGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTGAAATTTGTGGTTCTTA 1983
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                                                                                                                                                                                                                           254 TTTTTIGTATTTTTATGATGTTCGTTTTTTTAATGGATAATAAATTTTTTGTGTAATATTG 313
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                                                                              Sequence 834303, Application US/09925065A

Publication No. US2040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G:

ITTLE OF INVENTION: Noticetide Polymorphisms in the Human Genome

TITLE OF INVENTION: Noticetide Polymorphisms in the Human Genome:

TITLE OF INVENTION: Noticetide Polymorphisms in the Human Genome:

TITLE OF INVENTION: Noticetide Polymorphisms in the Human Genome:

TITLE OF INVENTION: Noticetide Polymorphisms in the Human Genome:

TITLE OF INVENTION: Noticetide Polymorphisms in the Human Genome:

FILE REPRENCE: 108027.135

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,147

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

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1.7%; Score 49.8;
Best Local Similarity 51.7%; Pred. No. 3.:
Matches 140; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                     2044 GCAATGCTTTTGCAAATAT 2062
                                                                                                                                                                                                                                                                                                                                                                                314 TAATTTTTATAGTAGTTTT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-925-065A-834303
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       1924
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sgeuence 66, Application US/10240708

publication No. US20050282157A1

general INFORMATION:

publication No. US20050282157A1

general INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: OLENIN, Kurt

TITLE OF INVENTION: Dy Assessing DNA Methylation

TITLE OF INVENTION: Dy Assessing DNA Methylation

FILE OF INVENTION: Dy Assessing DNA Methylation

FILE OF INVENTION: Dy Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/240,708

CURRENT FILING DATE: 2002-10-03

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR PILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR PILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01
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                                                                                                                                                1796 GTATCGCCTGAȚAGATTGTGTTATACGTTAACCTTTTTTTTTCTTACTGTTACTTTCAGTTC 1855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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1.7%; Score 50.2; DB 8; Length 5360;
Best Local Similarity 47.3%; Pred. No. 5.2;
Matches 151; Conservative 0; Mismatches 168; Indels 0
Score 50.8; DB 6; Length 664;
Pred. No. 2.2;
1; Mismatches 153; Indels
   Query Match
Best Local Similarity 48.0%;
Matches 142; Conservative
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RESULT 14

US-10-240-708-47

is Sequence 47, Application US/10240708

sequence 47, Application US/10240708

sequence 47, Application No. US20050282157A1

GENERAL INFORMATION:
TAPLICANT: OFFER, Alexander

APPLICANT: DISPERSENCK, Christian
APPLICANT: DISPERSENCK, Christian
APPLICANT: DISPERSENCK, Christian
APPLICANT: DISPERSENCY, Christian
APPLICANT: DISPERSENCY, Christian
APPLICANT: DISPERSENCY, Christian
APPLICANT: DISPERSENCY, Christian
FILE REFERENCE: 5013.1012
CURRENT FAPLICATION NUMBER: US/10/240,708

CURRENT FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR PRILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                         1353 AACCTCACCATATTTTGGAAGATTCCTACTCCATTTGCAAGTCATGCTTTTCACCCTATTG 1294
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                                                                                             2317 TCTCCATTTGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2437 ACGGGATACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGCCCGATTCATCTCA
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                                                                                                                                                                                                                                                                                     2377 AATGGTGACTTCTTTACTTGATGTTTTTCGGGTTTTTCAGGGCTCGCATTCCATCCGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1233 iggrrrairiaagicigiacaicifggrraaraiciggacaarrrccaircaiga 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 7.3;
0; Mismatches 117; Indels
Mismatches 116; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 50.4%;
Matches 119; Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-240-708-47
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LOCATION: (67, 20
    Matches 119;
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    TITLE OF INVENTION: Identification and Mapping of Single ITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49.4; DB 8; Length 2409;
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.7%; Score 49.4; DB 6; Length 613; Best Local Similarity 51.3%; Pred. No. 4; Matches 139; Conservative 1; Mismatches 127; Indels
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                                                                TITLE OF INVENTION: NULLECTURE COURTENT APPLICATION NUMBER: US/09/925,065A CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24 PRIOR PLING DATE: 2000-11-20 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR FILING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: US 60/261,766 PRIOR FILING DATE: 2001-01-16 PRIOR PILING DATE: 2001-01-16 PRIOR PILING DATE: 2001-01-16 PRIOR PILING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 957086 SEQ ID NO 934302 LENGTH: AT ALLIA COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED COURTED 
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Publication No. US20050255114A1
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ORGANISM: Homo sapiens
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US-09-925-065A-834302
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Best Local Similarity
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1.7%; Score 49.4; DB 12; Length 10166;
Best Local Similarity 49.4%; Pred. No. 8.9;
Matches 128; Conservative 0; Mismatches 131; Indels 0;
RESULT 15
US-11-147-606-3
Sequence 3, Application US/11147606
Sequence 3, Application US/11147606
Publication No. US20050278795A1
GENERAL INFORMATION:
APPLICANT: Miyazaki, Makoto
TITLE OF INVENTION: Stearoyl-CoA desaturase 4 gene
FILE REFERENCE: 960296.00197
CURRENT APPLICATION NUMBER: US/11/147,606
CURRENT APPLICATION NUMBER: 60/578,234
PRIOR APPLICATION NUMBER: 60/578,234
PRIOR PILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 10166
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CORGANISM: Mus musculus
US-11-147-606-3
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